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Perfect score:
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Listing first 45 s
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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 protein search, using sw model
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length: 2000000000
Match
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Gapop 10.0 , Gapext 0.5
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50
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A35644
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F72378
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T07366
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C;Date: 07-Jun-1996 #sequence-revision 07-Jun-1996 #text_change 18-Feb-2000
C;Accession: I54519, JC23662; PH1295
R;De Smet, C;; Lurquin, C;; van der Bruggen, P;; De Plaen, E;; Brasseur, F.
                                                                                                                                                                                                                                                                                                                                                                                                     melanoma antigen MAGE-12 - human
N;Alternate names: MAGE 21 protein
C;Species: Homo sapiens (man)
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#### ALIGNMENTS

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Immunogenetics 39, 121-129, 1994
A;Title: Sequence and expression pattern of the human MAGE2 gene.
A;Reference number: I54519; MUID:94102805
A;Status. A:Molecule type: mRNA A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN> A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN> A;Experimental source: melanoma cell line DM150; MAGE-12f R:Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van P. J. Exp. Med. 176, 1453-1457, 1992 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytoly A;Reference number: PH1294; MUID:93018875 A;Accession: PH1294; RESULT B96652 A;Cross-references: GB:L18877; NID:g499345; PIDN:AAA19023.1; PID:g499346 R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G. Biochem. Biophys. Res. Commun. 202, 549-555, 1994 A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935
A;Accession: JC2362 A;Map position: Xq28-Xq28 C;Superfamily: tumor associated protein MAGE F;168-176/Region: HLA-Al binding #status predicted A;Gene: GDB:MAGEA12; MAGE12; MAGE-12f A;Cross-references: GDB:331129 A; Molecule type: DNA A; Residues: 168-176 <TRA> A; Molecule type: DNA A; Residues: 1-314 <DES> protein F23N19.5 [imported] C; Genetics: A; Experimental source: MAGE-21 A; Status: preliminary; translated from GB/EMBL/DDBJ Query Match Best Local Matches 169 1 VVRIGHLYIL 10 VVRIGHLYIL 178 10; Similarity Conservative 100.0%; Arabidopsis thaliana 0; Score 50; DB 2 Pred. No. 0.02; Mismatches DB 2; Length 314; 0; Indels 0 Gaps 0;

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96652
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: B96652
A;Accession: B96652
A;Accession: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:L18920; NID:g436180; PIDN:AAA17729.1; PID:g436181 R;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, J. Exp. Med. 176, 1453-1457, 1992 Le: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-Al A; Accession: PH1294; MUID:93018875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    melanoma antigen MAGE-2 - human
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 18-Feb-2000
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A; Residues: 1-233 <STO>
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Best Local Similarity
""" By Conserve
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A; Residues: 168-176
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A;Molecule type: DNA
A;Residues: 1-314 <RES>
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A;Cross-references: GDB:273684
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Pred. No. 8.3;
0; Mismatches
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CDP-diacylglycerol synthetase-like protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: G8525 #text_change 16-Feb-2001 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Map position: 4
A; Introns: 25/3; 110/2; 161/1; 208/2; 260/3; 276/3; 305/3; 348/3; 367/3; 395/3
A; Note: T10I14.170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDP-diacylglycerol synthetase homolog T10I14.170 - C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 C;Accession: T04915
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A; Accession: T04915
A; Molecule type: DNA
A; Residues: 1-423 <BEV>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
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A; Residues: 1-423 <STO>
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A;Reference number: A85001; MUID:20083488
                                                                                                                                                                                                                                     CDP-diacylglycerol synthetase homolog F2401.17 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001 C:Accession: T01455
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                                        A,Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-427 <SHI>
                                                                                                                              submitted to the EMBL Data Library, January 1998 A; Description: Genomic sequence for Arabidopsis A; Reference number: Z14211
                                                                                                            A; Reference number: A; Accession: T01455
                                                                                                                                                                                               R;Shinn, P.; Buehler, eologis, A.; Ecker, J.
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nces: EMBL:AC003113; NID:g2689438; PID:g2781361 source: cultivar Columbia
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2; Mismatches
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C:Genetics:
A:Map position: 1
A:Map position: 1
A:Introns: 25/3; 110/2; 161/1; 208/2; 260/3; 276/3; 305/3; 348/3; 373/3; 401/3
A:Note: F2401.17
                                                                                                                                                                                                                                      R;Meijer, W.J.; Venema, G.; Bron, S.
Nucleic Acids Res. 23, 612-619, 1995
A;Title: Characterization of single strand origins of cryptic rolling-circle A;Reference number: I40549; MUID:95206941.
A;Reference number: I40565
A;Recession: I40565
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: I-305 <RESS
A;Cross-references: EMBL:U32380; NID:g1049123; PIDN:AAC44422.1; PID:g1049128
A;Experimental source: plasmid pTA1060
C;Genetics:
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A; Gene: SCOEDB: SCJ9A. 05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-234 <HAR>
A;Cross_references: EMBL:AL109972; PIDN:CAB53266.1; GSPDB:GN00070; SCOEDB:SCJ9A.05c
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A;Accession: T37141
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             pothetical protein 4.60 - Bacillus subtilis plasmid pTA1060 Species: Bacillus subtilis Plasmid pTA1060 Plate: 12-Aug-1996 #server-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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Best Local
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ecies: Streptomyces coelicolor
ate: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                       197
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                                       VLIGHVYVL 205
                                                                         VRIGHLYIL 10
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5; Conserv
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                                                                                                                                                                                                      subtilis plasmid pTA1060 hypothetical protein
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77.8%;
                                                                                                                               70.0%;
                                                                                                             Score 35; DB Pred. No. 20; 2; Mismatches
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Pred.
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Mismatches
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                                                                                                                                                 Length 305
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A;Description: specifically catalyzes the hydroxylation of medium chain saturated fat C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: chromoprotein; fatty acid metabolism; heme; iron; metalloprotein; oxidore
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                                                                         A; Gene:
                                                                                               C; Genetics:
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                                                                                                             A; Experimental source:
                                                         Function
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Best Local
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Matches

Local Similarity hes 6; Conser 1 VVRIGHLY 8

70.0%;

Score 35; DB Pred. No. 22; 1; Mismatches

2

Length 325

0

0

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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.P.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Febret, C.; Ferrari, Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galiech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Tanaha, T.; Terpstra, P.; Tognoni, A.; Tosatot, V.; Uchiya T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A, Jitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A.; Reference number: A69580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein yopk - Bacillus subtilis phage SPBc2 C; Species: Bacillus subtilis phage SPBc2 C; Species: Bacillus subtilis phage SPBc2 C; Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 20-Jun-2000 C; Accession: T12852; H69917 R; Lazarevic, V.; Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, submitted to the EMBL Data Library, August 1997 A; Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac A; Reference number: Z17583
A;Gene: yopR
C;Superfamily: Bacillus
                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: H69917
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                                                                                                                                                 A; Experimental source: strain
                                                                                                                                                                                              A;Cross-references:
                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-325 < KUN>
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                                                                                          Genetics:
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                                                                                                                                                                                                                                                                                                                           acid sequence not shown;
                                                                                                                                                 GB:Z99114; GB:Z99115; GB:AL009126; ce: strain 168
subtilis phage SPBc2 hypothetical protein
                                                                                                                                                                                                                                                                                                                                     translation
                                                                                                                                                                                         NID:g2634478; PIDN:CAB13997.1;
                                                                                                                                                                                                                                                                                                                                     not shown
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     yopR
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A;Molecule type: mRNA
A;Residues: 1-505 <CAB>
A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1;
                                                                                                                                                                                                                                                                                                                                                     cytochrome P450 (EC 1.14.-.-) 81B1c - Jerusalem artichoke
C;Species: Helianthus tuberosus (Jerusalem artichoke)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
T10896
                                                                                                                                                                                      R;Cabello-Hurtado, F.; Batard, Y.; Salaun, J.; Durst, F.; Pinot, F.; Werck-Reichhart, J. Blol. Chem. 273, 7260-7267, 1998
A;Title: Cloning, expression in yeast and functional characterization of CYP81B1, a p A;Reference number: Z17204; MUID:98184826
                                                                                                                                                A; Reference number: A; Accession: T10896
                                                                                                               A; Status: preliminary; translated
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                                                                                                                      from GB/EMBL/DDBJ
                  PID:g3059129
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CV.

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GcpE protein [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C;Accession: C86537
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F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcpE protein CP0383 [imported] - Chlamydophila pneumoniae (strains CWL029 and
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: E72087; D81582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:BA000008; NID:g8978745; PIDN:BAA98581.1; A;Experimental source: strain J138
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A; Residues: 1-613 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 28, 2311-2314, 2000
A-Title: Comparison of whole genome sequences of chlamydia beference number: A86491; MUID:20330349
Accession: C86537
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                                                                                          A;Cross-references: GB:AE002200; GB:AE002161; A;Experimental source: strain AR39, HL cells C;Genetics:
                                                                                                                                                                                 Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis A;Reference number: A81500; MUID:20150255
A;Accession: D81582
                                                                                                                                                                                                                                                                                                                                                                                                                     R; Kalman, S.; Mitchell, W.; Marathe, R.; Nature Genet. 21, 385-389, 1999
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                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-613 < REA>
                                                                                                                                                                                                                                                      A; Experimental source: strain CWL029
R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.;
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.
                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE001621; GB:AE001363; NID:g4376641; PIDN:AAD18517.1; PID:g43766
                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-613 <ARN>
                                                                         A; Gene: gcpE; CP0383
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; H.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987
A;Accession: H70535
                                                                                                                                                                                                                   A; Nolecule type: DNA
A; Nolecule type: DNA
A; Residues: 1-481, 'RT', 484-728 <SE2>
A; Residues: 1-481, 'RT', 484-728 <SE2>
A; Residues: 1.481, 'RT', 484-728 <SE2>
A; Residues: 1.481, 'RT', 484-728 <SE2>
A; Residues: 1.481, 'RT', 484-728 <SE2>
A; Riddener, K. M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, R.; Weidener, Sci. U.S.A. 88, 7001-7005, 1991
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A; Title: Evidence for the identity of human scatter factor and human hepatocyte growt
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C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A;Bescription: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JU0333
A;Accession: JU0333
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C;Superfamily: Mycobacterium tuberculosis hypothetical protein
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C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33312; A39006; PH0114;
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33312; A39006; PH0114;
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A36677; A35006; PH0114;
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A36677; A39006; PH0114;
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A
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A; Residues: 1-637 <COL>
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A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936 R;Seki, T.; Thara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asam Biochem. Biophys. Res. Commun. 172, 321-327, 1990
                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-728 <WEI>
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A; Residues: 1-728 <SEK>
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ce: strain H37Rv
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3; Mismatches
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R; Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Blochem. Blophys. Res. Commun. 175, 660-667, 1991
A; Tittle: Identification of the N-terminal residue of the heavy chain of both A; Reference number: PHO114; MUID:91207365
A; Recession: PHO114
A; Molecule type: protein
A; Residues: 32-43;53-58 <70S>
A; Experimental source: plasma
R; Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990
A; Title: Scatter factor: molecular characteristics and effect on the invasive A; Reference number: A37796; MUID:91035621
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A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,
A;Residues: 7: Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.;
R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.;
Ture 342, 440-443, 1999
                                                                                                                                                                                                           A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N. Eur. J. Biochem. 197, 15-22, 1991
                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-288,'ET' <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: the authors translated the codon CAG for residue 727 as Glu A; Note: part of this sequence, including the amino end of both the alpha and beta R; Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth.
                                                                                                                            A; Reference number: S15443; MUID:91200041
A; Accession: S15443
                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A; Accession: I59214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        itle: Molecular cloning and expression of human hepatocyte growth factor.
Reference number: S06794; MUID:90066676

A;Accession: S06794

A;Molecule type: mRNA
A;Residues: 1-31,'HK',34-77,'N',79-292,'Y',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
A;Experimental source: 11yer

A;Experimental source: 11yer
                  A; Cross-references:
                                                                                                       A;Status: preliminary
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A;Experimental source: embryonic lung
v · Arakaki, N.; Naka, D.;
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A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatoc; A;Reference number: A39006; MUID:91110540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-161,167-728 < RUB>
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A;Experimental source: leukocyt.
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; CBiochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA A;Reference number: A33512; MUID:89392017
A;Accession: A33512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Isolation and expression of cDNA
A;Reference number: A36677; MUID:91025062
A;Accession: B36677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A39006
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                                       ;Molecule type: mRNA;Residues: 1-288,'ET' <MIY2>
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sidues: 1-728 <MIY>
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               EMBL: X57574;
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            NID: 932083; PIDN: CAA40802.
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      PID: g32084
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                                                      A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-728 < Tas>
A; Residues: 1-728 < Tas>
A; Cross-references: GB:D90102; GB:M32987; NID:g220766; PIDN:BAA14133.1;
A; Note: the authors translated the codon GAG for residue 70 as Gln, GAC
R; Okajima, A.; Miyazawa, K.; Kitamura, N.
Buchem. 193, 375-381, 1990
A; Title: Primary structure of rat hepatocyte growth factor and induction
A; Reference number: S13211; MUID:91031482
A; Accession: S13211
                                 A; Description:
                                                                                                                                                                       A; Molecule type: mRNA
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Biochem.
A;Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A35644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F; 1-31/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                              stimulates
   have
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proteinase
                              mitosis
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F:128-206/Domain: kringle homology <KR1>
F:211-288/Domain: kringle homology <KR2>
F:305-383/Domain: kringle homology <KR3>
F:391-469/Domain: kringle homology <KR4>
F:495-728/Domain: beta chain #status experimental <BCH>
F:495-728/Domain: trypsin homology <TRY>
F:495-716/Domain: trypsin homology <TRY>
                                                                                                                               F;32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) F;294,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status F;487-604/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: alternative splicing; glycoprotein; growth factor; heterodimer;
                                                                                                                                                                                                                                                                                                                                                                         F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-494,495-728/Product: hepatocyte growth factor #status experimental
F;32-494/Domain: alpha chain #status experimental <ACH>
F:32-494/Domain: alpha chain #status experimental <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7g21.1-7g21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1;
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Finmor cytotoxic fact
Tumor: 152253; }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary; translated from GB/EMBL/DDBJ
  Similarity 50.05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    stimulates mitosis of hepatocytes and other cells
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53; MUID:92062058
                               70.0%;
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heterodimer
                               Score 35;
Pred. No.
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                                                     Length 728
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R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expres A;Reference number: A35644; MUID:90222197 C;Species: Rattus norvegicus (Norway rat) C;Date: 28-Sep-1990 #sequence\_revision 18-Nov-1992 hepatocyte growth factor precursor - rat N; Alternate names: hepapoietin A; scatter factor #text\_change 21-Jul-2000 expression of s.;

activity

precursor

induction

PID: g220767

for

residue

of

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C: Superfeatly: hepatocyte growth factor; kringle bomology; trypsin bomology; prysin bomology; crypsin bomology; crypsin bomology; prysin bomology; prysin bomology; prysin bomology; prysin bomology; prysin bomology; prysin bomology; provided data; predicted pr
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 20, 2001, 14:04:34 ; Search time 28.81 Seconds (without alignments) 21.152 Million cell updates/sec

Title: Perfect score: Sequence: US-09-692-401-6 42 1 RIGHLYIL 8

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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	TD.		rs -		hypothetical prote	voltage-gated pota	UDP-N-acetylmurama	probable phosphoma	CDP-diacylqlycerol	CDP-diacylqlycerol	٠-	hypothetical prote	protein F23N19.5 [			heterogeneous nucl		hepatocyte growth			se regul	melanoma antiqen M	hypothetical prote	probable retroelem	hypothetical prote	e.	_	melanoma antiqen M	Description	

RESULT

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1 RIGHLYIL 8 ||||||| 171 RIGHLYIL 178

cytochrome P450 (EC 1.14.-.-) 81Blc - Jerusalem artichoke

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30	30	30	30	30	30	30	30	30	30	30	Ω	ω 1	31	ω	31
71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	73.8	73.8	73.8	73.8	73.8
303	288	280	256	256	247	189	188	184	144	65	1530	1507	720	615	613
2	2	N	N	2	ν	N	2	N	N	N	N	N	N	N	N
C32252	G64000	A75614	JQ1106	S26742	S67685	A83573	T38223	T36644	G70023	A23783	I45944	A40228	E82384	C75278	E72087
gene V protein - A	hypothetical prote			tonoplast intrinsi	hypothetical prote	conserved hypothet	probable adenine p	_		hypothetical prote	neurexin I-alpha -	neurexin I-alpha p	ornithine decarbox	DNA polymerase III	gcpE protein CP036

# ALIGNMENTS

Query Match 100.0%; Score 42; DB 2; Length 314; Best Local Similarity 100.0%; Pred. No. 0.39; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Residues: 168-176 <tra> A;Experimental source: MAGE-21 C;Genetics: A;Gene: GDB:MAGEA12; MAGE12; MAGE-12f A;Cross-references: GDB:331129 A;Mage position: Xq28-Xq28 C;Superfamily: tumor associated protein MAGE F;168-176/Region: HLA-Al binding #status predicted</tra>	A;Molecule type: mRNA A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <din> A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <din> A;Experimental source: melanoma cell line DM150; MAGE-12f R;Traversari, C; van der Bruggen, P; Luescher, I.F.; Lurquin, C; Chomez, P.; Van P J. Exp. Med. 176, 1453-1457, 1992 A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytoly A;Reference number: PH1294; MUID:93018875 A;Accession: PH1295 A;Accession: PH1295 A;Molecule type: DNA</din></din>	A;Reference number: 154519; MUID:94102805  A;Accession: T54519 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-314 <des> A;Cross-references: GB:L18877; NID:9499345; PIDN:AAA19023.1; PID:9499346 R;Cling, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G. Biochem. Biophys. Res. Commun. 202, 549-555, 1994 A;Title: Cloning and analysis of MAGE-1-related genes. A;Reference number: JC2358; MUID:94311935</des>	RESULT 1  154519  melanoma antigen MAGE-12 - human N;Alternate names: MAGE 21 protein C;Species: Homo sapiens (man) C;Date: 07-Jun-1996 #sequence_revision(07-Jun-1996\#text_change 18-Feb-2000 C;Date: 07-Jun-1996 #sequence_revision(07-Jun-1996\#text_change 18-Feb-2000 C;Accession: 154519; JC2362; pH1295 C;Accession: 154519; JC2362; pH1295 C;Accession: 154519; JC2362; pH1295 C;Accession: 154519; JC2362; pH1295 A:Timmunogenetics 39, 121-129, 1994 A:Title: Sequence and expression mattern of the human MAGE Topic A:Title: Sequence and expression mattern of the human MAGE Topic
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C;Species: Helianthus tuberosus (Jerusalem artichoke)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C;Accession: T10896
R;Cabello-Hurtado, F.; Batard, Y.; Salaun, J.; Durst, F.; Pinot, F.; Werck-Reichhart, D.
J. Biol. Chem. 273, 7260-7267, 1998
A;Title: Cloning, expression in yeast and functional characterization of CYP81B1, a plan
A;Reference number: Z17204; MUID:98184826
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <CAB>
A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1; PID:g3059129
A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1; PID:g3059129
A;Experimental source: cv. blanc commun
C;Genetics:
A;Gene: CYP81B1C
C;Function:
A;Description: specifically catalyzes the hydroxylation of medium chain saturated fatty
C;Superfamily: human cytochrome P450 romology cytochrome P450 homology
C;Keywords: chromoprotein; fatty acid metabolism; heme; iron; metalloprotein; oxidoreduc
F;301-465/Domain: cytochrome P450 homology <P45>
F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                    hypothetical protein T2L5.9 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 C;Accession: T01956 R;Geisel, C.; Smith, A.; Le, T. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of A. thaliana T2L5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T37141
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A;Accession: T37141
A;Status: preliminary; translated
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A; Residues: 1-234 <HAR>
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                                           A; Reference number: A; Accession: T01956
                                                                A; Description: The sequence of A; Reference number: Z14470
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  A;Status: t
A;Molecule
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translated from type: DNA
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                         GB/EMBL/DDBJ
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August 1999
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A;Residues: 1-1244 <GEI>A;Cross-references: EMBL:AF096371; NID:g3695386; A;Experimental source: cultivar Columbia C;Genetics:
                                                                                                                                                                                                                                                                                                                      hypothetical protein 4.60 - Bacillus subtilis plasmid C;Species: Bacillus subtilis C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #te
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A;Map position: 2
C;Superfamily: retrovirus-related polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: E84589
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A; Introns: 75/1;
A; Note: T2L5.9
A; Genome: plas
C; Superfamily:
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A;Accession: I40565
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A; Residues: 1-1461 <STO>
A; Cross-references: GB:A
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A;Accession: E84589
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Nucleic Acids Res.
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                                                                                         A; Residues: 1-305 < RES>
A; Cross-references: EMB
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                                                                   A; Experimental
                                                                                                                                  A; Molecule type: DNA
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Matches 6; Conserv
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                                                                     source:
Bacillus subtilis plasmid pTA1060 hypothetical protein
                                                                                                                                                                                                                                                       Venema, G.; Bron, S.
es. 23, 612-619, 1995
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                                                                   EMBL:U32380; NID:g1049123; PIDN:AAC44422.1; PID:g1049128
>e: plasmid pTA1060
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Pred. No. 83;
2; Mismatches
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Pred. No. 1e+02;
2; Mismatches
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C.Y

78.6%; 71.4%;

Score Pred. No. ДВ 28;

2;

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glucokinase regulator - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: $48729; $49339
R:Velga-da-Cunha, M.; Detheux, M.; Watelet, N.; van Schaftingen, E.
Eur. J. Biochem. 225, 43-51, 1994
A:Title: Cloning and expression of a Xenopus liver cDNA encoding a fructose-A; Reference number: $48729; MUID:95010134
A:Accession: $48729
A:Status: preliminary
A:Mccession: $48729
A:Status: preliminary
A:Mclecule type: mRNA
A:Residues: 1-619 <VEID
A:Cross-references: EMBL:X80901; NID:g556677; PIDN:CAA56863.1; PID:g556678
C:Superfamily: glucokinase regulator
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C;SpecLes: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 18-Feb-2000
C;Accession: JC2361; PH1296; I38438
R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: tun F; 168-176/Region:
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melanoma antigen MAGE-3 - human
melanoma antigen MAGE 3 protein
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A; Residues: 1-314 < RES>
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A; Residues: 168-176 < TRA>
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Score 33;
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                  Length 619;
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A; Residues: 1-728 <MIY>
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A; Residues: 1-728 <SE3>
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A; Residues: 1-728 <WEI>
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2, 213-219, 1991
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A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846 R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991 A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a varia; Reference number: A39006; MUID:91110540 A;Accession: A39006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-161,167-728 <SE4>
A; Cross references: EMBL: X16323
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R;Seki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya Biochem. Biophys. Res. Commun. 1321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth fa A;Reference number: A36677; MUID:91025062
A;Accession: B36677;
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A;Residues: 1-728 <SEK>
A;Cross-references: DDBJ:D90318
A;Coss-references: DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as
A;Note: the authors translated the codon GAA for residue 662 as
A;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, (
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A;Accession: JH0579
R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, Biochem. Biophys. Res. Commun. 175, 660-667, 1991 A;Title: Identification of the N-terminal residue of the heavy A;Reference number: PHO114; MUID:91207365
                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-161,167-728 <RUB>
A;Cross-references: GB:M55379
A;Experimental source: embryonic lung
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R;Miyazawa, K; Tsubouchi, H; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nak
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth
A;Reference number: A33512; MUID:89392017
A;Accession: A33512
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A; Residues: 1-481, 'RT', 484-728 <SE2>
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C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JU0333; A41140; B36677; A36677; A33512; A39006; PH0114;
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
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S.
                                                                                                         S.; Kondo, J.; Nakayam
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A; Accession: PHO
A; Molecule type:
A; Residues: 32-4
A; Experimental s
A:Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Roywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F;1-31/Domain: signal sequence #status predicted <SIG>
F;32-494,495-728/Product: hepatocyte growth factor #status experimental <MAT>
F;32-494/Domain: alpha chain #status experimental <ACH>
F;128-206/Domain: kringle homology <KR1>
F;211-288/Domain: kringle homology <KR3>
F;305-383/Domain: kringle homology <KR3>
F;305-383/Domain: kringle homology <KR3>
F;391-469/Domain: kringle homology <KR3>
F;391-469/Domain: kringle homology <KR3>
F;391-469/Domain: kringle homology <KR4>
F;495-728/Domain: kringle homology <KR4>
F;495-718/Domain: beta chain #status experimental <BCH>
F;495-716/Domain: trypsin homology <KR4>
F;394-402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;487-604/Disulfide bonds: #status predicted
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A;Residues: 1-288/ET/SHAP>
A;Residues: 1-288/ET/SHAP>
A;Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
R;Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
Bur. J. Biochem. 197, 15-22, 1991
A;Title: An alternatively processed mRNA generated from human hepatocyte growth factor
A;Reference number: S15443; MUID:91200041
A;Accession: S15443; MUID:91200041
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A;Note: part of this sequence, including the amino end of both the alpha and beta chains
R;Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
A;Reference number: I59214; MUID:93087571
A;Accession: I59214
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A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
A;Experimental source: liver
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A;Accession: A37796
A;Accession: Type: protein
A;Molecule type: protein
A;Molecule: 86-91;329-344;356-363,'xx',366-370;425-434;442-447,'x',449-450;543-546,'x'
A;Residues: 86-91;329-344;356-363,'xx',366-370;425-434;442-447,'x',449-450;543-546,'x'
R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tas
Nature 342, 440-443, 1989
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A;Residues: 1-288, 'ET', 'MIY2>
A;Cross-references: EMBL:x57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
A;Cross-references: EMBL:x57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
R;Shima, N.; Nagao, M.; Ogakl, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Blochem. Blophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
A;Reference number: I52253; MUID:92062058
A;Reference number: I52253; MUID:92062058
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A;Cross-references: GDB:127524; OMIM:142409
A;Map position: 7q21.1-7q21.1
A;Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; C;Complex: disulfide-bonded heterodimer of chains derived C;Function:
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C;Genetics:
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A; Residues: 161-166 <SHI>
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: 32-43;53-58 <YOS>
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A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC R;Okajima, A.; Miyazawa, K.; Kitamura, N. Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction A;Reference number: S13211; MUID:91031482
A;Accession: S13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;56-495/Product: hepatocyte growth factor #status predicted <ACH>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;121-289/Domain: kringle homology <KR2>
F;301-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR3>
F;496-728/Domain: kringle homology <KR4>
F;496-728/Domain: kringle homology <KR4>
F;496-728/Domain: krypsin homology <KR4>
F;496-719/Domain: trypsin homology <TRY>
F;496-719/Domai
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C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer;
F; 1-32/Domain: signal sequence #status predicted <SIG>
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Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of
A;Reference number: A35644; MUID:90222197
A;Accession: A35644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hepatocyte growth factor precursor - rat N; Alternate names: hepapoietin A; scatter factor
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A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same pr
hepatocyte growth factor precursor - mouse
N;Alternate names: hepapoietin A; scatter factor
C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
C;Accession: JC2117; pc2064; A60185; S43416; S45521; S17173; S10966; I48758;
R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enaml, J.
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Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000;

Accession: A35644; S13211
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Pred. No.
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R; Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.

Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

A; Title: Purified scatter factor stimulates epithelial and vascular endothelial cell mig
A; Reference number; A60185; MUID:90377927

A; Accession: A60185

A; Molecule type: protein
A; Residues: 'X',184-188,'KX',191-192,'X',194,'XX',197;357-364,'XX',367;375-377,'E',379,'
R; Liu, Y; Michalopoulos, G.K.; Zarnegar, R.
Biochim. Biophys. Acta 1216, 299-303, 193
A; Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth
A; Reference number: S43416; MUID:94060105
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-728 <LIUD
A; Cross-references: EMBL:X72307
R; Liu, Y.
A;Ittle: Hepatocytes and scatter factor.
A;Reference number: $10966; MUID:90326152
A;Recession: $10966
A;Recession: $10966
A;Recession: $10966
A;Recession: $10966
A;Status: preliminary
A;Molecule type: protein
A;Residues: $496-507, 'x', 509-512, 'L', 514-516, 'x', 518-519 <NAT>
A;Molecule type: protein
A;Residues: $496-507, 'x', 509-512, 'L', 514-516, 'x', 518-519 <NAT>
A;Molecule type: protein
A;Residues: $496-507, 'x', 509-512, 'L', 514-516, 'x', 518-519 <NAT>
A;Molecule type: DAG
A;Pitle: Characterization of the scatter factor/hepatocyte growth fac
A;Reference number: $148758; MUID:95122532
A;Reference number: $148758; MUID:95122532
A;Recession: $148758; MUID:95122532
A;Recession: $148758; MUID:95122532
A;Rocession: $148758; MUID:9512253
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A; Reference number: $45521
A; Accession: $45521
A; Accession: $45521
A; Accession: RNNA
A; Residues: 1-563, 'H', 565-728 <LI2>
A; Cross-references: EMBL:X72307
R; Coffer, A.; Fellows, J.; Young, S.; Pappin, Blochem. J. 278, 35-41, 1991
A; Title: Purification and characterization of A; Reference number: $17173; MUID:91354223
A; Accession: $17173
A; Molecule type: protein
A; Residues: 496-517, 'T', '519 <COF>
R; Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A; Title: Uncertain A; Molecule type: protein
A; Residues: 496-517, 'T', 519 <COF>
R; Gherardi, E.; Stoker, M.
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A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as A;Reference number: JC2117; MUID:94183257
A;Accession: JC2117
A;Molecule type: mRNA
A;Residues: 1-728 <SAS2>
A;Cross-references: GB:D10212; NID:9220435; PIDN:BAA01064.1; PID:9220436
A;Experimental source: fibroblast, COS-1 cell
A;Note: submitted to JIPID, May 1993
A;Accession: PC2064
A;Molecule type: protein
A;Residues: 496-504 <SA22>
A;Residu
                                                                                                                       ;Note: does not have proteinase activity;
Superfamily: hepatocyte growth factor; kringle homology; trypsin homology;
[Reywords: alternative splicing; glycoprotein; growth factor; heterodimer;
]1-32/Domain: signal sequence #status predicted <SIG>
]56-495,496-728/Product: hepatocyte growth factor #status predicted <MAT>
[56-495/Domain: kringle homology <KRI>
]212-289/Domain: kringle homology <KRI>
]223-289/Domain: kringle homology <KRI>
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N;Alternate names: hnRNP F; nucleolin-like process. C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text
C;Accession: S43484; A42005
C;Accession: S43484; A42005
R;Matunis, M.J.; Xing, J.; Dreyfuss, G.
Nucleic Acids Res. 22, 1059-1067, 1994
A;Title: The hnRNP F protein: unique primary structure, A;Reference number: S43484; MUID: 94203790
A;Accession: S43484
A;Ccession: S43484
                                                             A. Molecule type: mRNA
A. Molecule type: mRNA
A. Residues: 1-415 <MATY
A. Residues: 1-415 <MATY
A. Gross-references: GB:L128010; NID:g452047; PIDN:AAC37584.1; PID:g452048
A. Gross-references: GB:L128010; NID:g452047; DID:g452048
A. Mote: it is uncertain whether Met-1 or Met-2 is the initiator
R. McDonald, H.; Smailus, D.; Jenkins, H.; Adams, K.; Simpson, N.E.; Good:
Genomics 13, 344-348, 1992
A. Fitle: Identification and characterization of a gene at D10S94 in the JA; Reference number: A42005; MUID:92307667
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F:33/Modified site: pyrrolidone carboxylic acid (Gln) (in matu F:295,403,559,655/Binding site: carbohydrate (Asn) (covalent) F:488-607/Disulfide bonds: #status predicted
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C;Superfamily: probable hexosyltransferase
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A; Molecule type: mRNA
A; Residues: 2-415 <MC
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                                                         A; Reference number: A; Accession: A42005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-350 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 399,
                                     A; Status: not compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            heterogeneous
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11 RIGHLLIM 18
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5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          nuclear ribonucleoprotein F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Clayton, R.A.;
Stewart, A.M.; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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75.0%;
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62.5%;
                                       conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Gill, S.R.; (Cotton, M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB
Pred. No. 74;
2; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NID:g4981144;
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                                                                                                                                           Simpson, N.E.; Goodfellow, P.J
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; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                              nucleic
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A;Cross-reterences: Obliveira, M.A.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak R.G.; Niger, R.C.; Niger, M.C.; de Rosa, A.C.; de Sa, R.C.; Santelli, R.C.; M.S.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Aprice, A.J.S.; Elenach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Canargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.; Ducena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.; Santelli, R.C.; Frohm sa, Nuthors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, W.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu Chado, M.A.; Madeira, M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.A.; Althors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nupes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodriques, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Honore, B.; Rasmussen, H.H.; Vorum, H.; Dejgaard, K.; Liu, X.; Gromov, P.; Madsen, P.; J. Biol. Chem. 270, 28780-28789, 1995
A;Title: Heterogeneous nuclear ribonuclearproteins H, H', and F are members of a ubiquit A;Reference number: A57806; MUID:96081943
A;Accession: I39358
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-449 < RES>
A;Residues: 1-449 < RES>
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heterogeneous nuclear ribonucleoprotein H - human
N;Alternate names: 49K protein; hnRNP H
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: 139358
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A;Gene: GDB:HNRPF
A;Cross-references: GDB:5429144; OMIM:601037
A;Map position: 10q11.21-10q11.22
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                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: E82849 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conserved hypothetical protein xF0095 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Aylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: E82849
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
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A;Cross-references: GDB:5428597; GDB:626033; OMIM:601035
A;Map position: 5q35.3-5q35.3
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                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE003863; GB: AE003849; NID: g9104863; PIDN: AAF82908.1; GSPDB: GN00
                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-101 <SIM>
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Best Local :
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Best Local :
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6; Conserv
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6; Conser
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85.7%;
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85.7%;
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Pred. No.
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64;
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A;Gene: XF0095
C;Superfamily: Methanococcus jannaschii conserved
                                                                                                        A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A;Reference number: A59328
                                                          C; Genetics:
                                                                                     A; Contents: annotation
                                     XF0095
                hypothetical protein
                  мJ0652
                                                                                                                                                Silv
A.L.
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Qy
                                  Matches
                                         Query Match
Best Local
79
               1 RIGHLYIL 8
RIGHIAIL 86
                                  Similarity 6; Conserv
                                  Conservative
                                           73.8%;
75.0%;
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                                           Score 31; DB Pred. No. 21;
                                    Mismatches
                                                    2;
                                                    Length 101;
                                    Indels
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                                    Gaps
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Search completed: June Job time: 82 sec 20, 2001, 14:04:35 Ъ

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Title:
Perfect score:
Sequence:
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Maximum DB seq
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Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
     protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 0
length: 2000000000
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Match
     BLOSUM62
Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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     DВ
  ROHI HUMAN
ROLZ HUMAN
C312_DROME
MAG2_HUMAN
MURC_BUCAI
PARE_BORBU
GYER_BARBA
TIPA_PHAVU
Y077_HAZIN
PQOB_ACICA
MAG6_HUMAN
TGT_ARCFU
CDS1_ARAFU
NEX3_HUMAN
C933_SOYBN
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•	Ĭ.,	-	008374 hyphomicrob	-		_	Q14012 homo sapien		-	_	-

### ALIGNMENTS

DR DR DR FTT TEN	88888888	% <b>₹</b> ₹₹₹\$	RA R	RESULT ID AC DT ODT DT 1 DT 1 DT 1 DT 1 DT 1 DT 0 DT 0 DT
MMIN; 300177; - AAA19023.1;  MIN; 300177; - InterPro; IPR002190;  Pfam; PF01454; MAGE; 1.  Antigen; Multigene family; Tumor antigen.  DOMAIN  CONFLICT  10  10  CONFLICT  10  CONFLICT  10  CONFLICT  107  CONFLICT  107  CONFLICT  107  CONFLICT  1087  107  CONFLICT  109  P > S (IN REF. 2).  CONFLICT  300  300  P -> S (IN REF. 2).  CONFLICT  300  300  P -> S (IN REF. 2).	his SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL he European Bioinformatics Institute. There are no restrict se by non-profit institutions as long as its content is codified and this statement is not removed. Usage by and fo ntities requires a license agreement (See http://www.isb-sib.r send an email to license@isb-sib.ch).	MEDLINE-944311935; PubMed-8037761; MEDLINE-944311935; PubMed-8037761; Ding M., Beck R.J., Keller C.J., Fenton R.G.; "Cloning and analysis of MAGE-1-related genes."; "Cloning and analysis of MAGE-1-related genes."; Biochem. Blophys. Res. Commun. 202:549-555(1994).  -i- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN TUMOR -i- TRANSFORMATION OR ASPECTS OF TUMOR PROGRESSION.  -i- TISSUE SPECIFICITY: EXXRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES.  -i- SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY (90%) WITH MAGE-2.	SEQUENCE FROM N.A.  SEQUENCE FROM N.A.  MEDLINE-94102805; PubMed=8276455;  de Smet C., Lurquin C., van der Bruggen P., de Plaen E., Brasseur F.,  Boon T.;  "Sequence and expression pattern of the human MAGE2 gene.";  Immunogenetics 39:121-129(1994).  [2]  SEQUENCE FROM N.A.	

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P43357;
01-NOV-1995
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Ding M., Beck R.J., Keller C.J., Fenton R.G.;

"Cloning and analysis of MACE-1-related genes.";

Biochem. Biophys. Res. Commun. 202:549-555(1994);

Biochem. Biophys. Res. Commun. 202:549-555(1994);

Biochem. Biophys. Res. Commun. 202:549-555(1994);

BIOCHEM. BIOPHYS. RES. COMMUN. THOUGH MAY PLAY A ROLE IN EMBRYONAL PUMOR FOR TUMOR ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS CYTOLYTIC T LYMPHOCYTES.

--- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SOUAMOUS CELL CARCINOMA, LUNG CARCINOMA, HEAD AND NECK SOUAMOUS CELL CARCINOMA, LUNG CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaugler B., van den Eynde B., van der Br
Gaforio J.J., de Plaen E., Lethe B., Bra
"Human gene MAGE-3 codes for an antigen
autologous cytolytic T lymphocytes.";
J. Exp. Med. 179:921-930(1994).
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                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN) (ANTIGEN MZ2-D).
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Eukaryota; Metazoa;
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MUTAGEN
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MIM; 300174; -.
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    2 IGHLYI 7
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n; Multigene family; Tumor antigen.
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170 170 D->*
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etazoa; Chordata;
cheria; Primates;
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170
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Pred. No. 0.21;
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Catarrhini;
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the B., Brasseur F., Boon T.;
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P14210;
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Mammalia; Eutheria;
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HGF OR HPTA.
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CKK.Abin...

CRACKARIAN

D GCKR XENLA

C 991754;

C 991754;

O1-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR).

OS Xenopus laevis (African clawed frog).

CE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Yenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001347; -.
InterPro; IPR001741; -.
Pfam; PF01380; SIS; 1.
PROSITE; PS01272; GCKR; 1.
SEQUENCE 619 AA; 68738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen "Cloning and expression of a Xenopus liver cDNA encoding a phosphate-insensitive regulatory protein of glucokinase."; Eur. J. Biochem. 225:43-51(1994).
SEQUENCE FROM N.A.
MEDLINE=91340155; PubMed=1831432;
Seki T., Hagiya M., Shimonishi M., Nakamura T.,
Seki T., Hagiya M. Shimonishi M., Nakamura T.,
"Organization of the human hepatocyte growth faw
                                                                                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
HEPATICCYTE GROWTH FACTOR PRECURSOR (SCATTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95010134; PubMed=7925465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - 1- SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
                                                                                                                                                                                                                  Homo sapiens (Human)
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Primates;
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Pred. No.
                                                                                                                                                                 Craniata; Vertebrata;
Catarrhini; Hominidae;
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Pred. No. 29;
Mismatches
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102:213-219(1991).

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TISSUB-Leukocyte;
REDLINE-91025062; PubMed-2145836;
MEDLINE-91025062; PubMed-2145836;
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MEDLINE-91025062; PubMed-2145836;
MEDLINE-91025062; Not State of Control of Medical 
                                                                                                                                                        MEDLINE-92331602; PubMed-1321034;
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EMBO J. 11:2503-2510(1992).
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Structure [10]
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Sugimura A., Tashiro K., Shimizu (
"Molecular cloning and expression
Nature 342:440-443(1989).
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Nakayama H., Gohda E., Kitamura
Hishida T., Daikuhara Y.;
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Proc. Natl. Acad.
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MEDLINE-91334393; PubMed-1831266;
Weidner K.M., Arakaki N., Hartmann G.,
Rieder H., Fonatsch C., Tsubouchi H., 1
                               Rubin J.S., Bottaro D.P., E
"The solution structure of
factor reveals a potential
                                                                                                                                                                                                                                                                                                                          Biochem.
                                                                                                                                                                                                                                                                                                                                                on the alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of the N-terminal residue of the heavy native and recombinant human hepatocyte growth factor." Biochem. Biophys. Res. Commun. 175:660-667(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL SEQUENCE CLEAVAGE SITE.
MEDLINE-91207365; PubMed-1826837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birchmeier W.; "Evidence for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                              STRUCTURE
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                                                                                                                                                                                                                                                                                                                           Biophys.
                  veals a potential heparin-binding
6:109-116(1998).
                                                                 54323; PubMed=9493272;
zzulla M.J., Kaufman J.D.,
Bottaro D.P., Byrd R.A.;
                                                                                                                            NMR OF
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PROSITE; PS50070; KRINGLE_2; 4.
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Structure 6:1383-1393(1998).
-!- FUNCTION: HGF IS A POTENT
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Best Local :
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CARBOHYD
CARBOHYD
                                                                                                                                                                                                 Q08048; Q64007; Q61662;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
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SEQUENCE FROM N.A.
TISSUE-Liver;
MEDLINE-94660105; PubMed-8241272;
Liu Y., Michalopoulos G.K., Zarne
                                                MEDLINE=94363381; PubMed=8081873;
Lee C.C., Kozak C.A., Yamada K.M.;
"Structure, genetic mapping, and expression
                                                                                                                          SEQUENCE FROM N.A., AND SE
TISSUE=Mammary fibroblast;
MEDLINE=94183257; PubMed=8
                                                                                                                                                              Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
                                            "Structure, factor gene
                                                                          TISSUE=Liver;
                                                                                 SEQUENCE FROM N.A.
                                                                                                Biochem.
                                                                                                       factor as hepatocyte growth factor.
                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                      IDJINE-94183257; pubMed-8135822;
ssaki M., Nishio M., Sasaki T., Enami J.;
seaki M., Nishio M., Sasaki T., Enami J.;
Identification of mouse mammary fibroblast-derived
                                                                                                                                                                                                                                                                                    1 RIGHLYIL
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5; Conserv
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Rodentia;
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                                                                                                                                                                                                                                                                                                               78.6%;
62.5%;
                                                                                               Commun. 199:772-779(1994).
                                                                                                                                          SEQUENCE
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QR -> HK
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N-LINKED (GLCNAC. . .) (PO
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Sciurognathi; Muridae; Murinae;
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SERINE PROTEASE-LIKE.
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(GLCNAC...)
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MGD; MGI:96079; Hgf.
Interpro; IPR000001; -.
Interpro; IPR001254; -.
Interpro; IPR001314; -.
Interpro; IPR003014; -.
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Pfam; PF00051; kringle; 4.
Pfam; PF00051; kringle; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS00021; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein; Serine protease homolog;
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DOMAIN
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EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth factor.";
Biochim. Biophys. Acta 1216:299-303(1993).

-I- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND AS GROWTH FACTOR FOR A BROAD SPECTBUM OF TISSUES AND CELL T IT HAS NO DETECTABLE PROTEASE ACTIVITY.

-I- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY DISULTIDE BOND.

-I- ALTERNATIVE PRODUCTS: A SHORT FORM OF HGF IS PRODUCED BY ALTERNATIVE RNA SPLICING. THE SEQUENCE SHOWN HERE IS THAT O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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between
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; D10212; BAA01064.1;
, D10213; BAA01065.1;
,; S71816; AAB31855.1;
,; X72307; CAA51054.1;
; P14210; 2HGF.
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33
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BELONGS TO
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          INTERCHAIN (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MISSING (IN SHORT ISOFORM).

N -> K (IN REF. 2).

V -> L (IN REF. 3).
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KRINGLE
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                              HEPATOCYTE GROWTH FACTOR ALPHA CHAIN HEPATOCYTE GROWTH FACTOR BETA CHAIN. PYRROLIDONE CARBOXYLIC ACID
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-> L (IN REF. 2)
-> H (IN REF. 3)
A0381FC497534328
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Similarity 5; Conser

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78.6%; 62.5%;

Score 33; DB Pred. No. 34; 2; Mismatches

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                                       PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein; Serine
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Pfam; PF00051; kring1a; 4.
Pfam; PF00089; trrpgs1a; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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EMBL;
PIR; S
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Okajima A., Miyazawa K., Kitamura N.;
"Primary structure of rat hepatocyte growth factor and induct its mRNA during liver regeneration following hepatic injury."
Eur. J. Biochem. 193:375-381(1990).
-I- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL.
                                                                                                                                                                                                                                InterPro; IPR000001; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR003014; -.
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Shimizu S., Nakamura T.;
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01-NOV-1990 (Rel. 16, Las
15-JUL-1998 (Rel. 36, Las
HEPATOCYTE GROWTH FACTOR
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SUBJUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY DISULFIDE BOUN SWILLARTTY: CONTAINS 4 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PETTIDASE FAMILY S1; ALSO KNOWN AS THERYPSIN FAMILY. PLASMINGEN SUBFAMILY.
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; X54400; CAA38266.1;
S13211; S13211.
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Rodentia;
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A HONOIRE B., RASMUSSEN H.H., VORUM H., Delgaard K., Liu X.,
A HONOIRE B., RASMUSSEN H.H., VORUM H., Delgaard K., Liu X.,
A Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.;
THE TABLE TO THE TRANSLATE THE TENDER THE TENDER TO THE HETEROGENOUS THE SPROTEIN (1995).

L. J. Biol. Chem. 270:28780-28789(1995).

C. -! FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BEST OF THE PROCESSING EVENTS THAT PRE-MRNAS IN THE CYTOPLASM. PROBABLY CONTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. PROBABLY CONTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM.

C. -!- SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.

C. -!- SUBCELLULAR LOCATION: STAPPRESSED UBIQUITOUSLY.

-!- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way as the content is in the same of the second content in the second content is in the second content in the second content is in the second content in the second content is in the second content in the second content is in the second content in the second content in the second content is in the second content in the second content in the second content is in the second content in the second content
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(See http://www.isb-sib.ch/announce,
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01-OCT-1996
01-OCT-2000
                         PIOTEIN database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).

-I- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN (HURNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYPOPLASM. BINDS POLY (RG)
-I- SUBCELLULAR LOCATION: NUCLEAR; NUCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honore B., Rasmussen H.H., Vorum H., Dejgaard K., Liu X., Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.; "Heterogeneous nuclear ribonucleoproteins H, H', and F are a ubiquitously expressed subfamily of related but distinct encoded by genes mapping to different chromosomes."; J. Biol. Chem. 270:28780-28789(1995).
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Aarhus/Ghent-2DPAGE;
MIM; 601037; -.
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MEDILINE-94203790; PubMed-7512260;
Matunis M.J., Xing J., Dreyfuss G.;
"The hnRNP F protein: unique primary structure, properties, and subcellular localization.";
Nucleic Acids Res. 22:1059-1067(1994).
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H (HN
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PROSITE; PS50102; RRM; 2.
PROSITE; PS00030; RRM, RN, 1;
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                            PARTIAL SEQUENCE FROM N.A.
MEDLINE=96081943; PubMed=7499401;
HONOTE B., Rasmussen H.H., Vorum H., Dejgaard K.,
Gromov P., Madsen P., Gesser B., Tommerup N., Cel.
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Aarhus/Ghent-2DPAGE;
Aarhus/Ghent-2DPAGE;
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Vorechovsky I., Vetrie D., H
Zhou J.N., Notarangelo L.D.,
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                                                                                                                                                                                    FROM
J.C.,
J.W.,
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RESULT 10 C312_DROME
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Best Local S
Matches 6
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J. Biol. Chem. 270:28780-28789(1955).

-I. FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG).

-I. SUBCELULULAR LOCATION: NUCLEAR; NUCLEOPLASM.
-I. TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-I. SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
STRAIN-BERKELEY;

MEDLINB-20196006; PubMed-10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.

Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
                                                                                                                                                                                                                                                                                                           01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PROBABLE CYPOCHROME P450 312A1 (EC 1.14.-.-)
CYP312A1 OR CG5137.
                                                                                                                                                                                                                                                                                                                                                                                                               C312_DR(
Q9VVN6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
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DOMAIN
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Pterygota; Neoptera; Endopterygota;
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                                                                                                                                                                    SEQUENCE
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RNA-BINDING (RRM) 1.
RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
2 X 16 AA GLY-RICH AF
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    Helt G., Nelson C.R., Miklos G.L.G.,
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MAG2\_HUMAN ID MAG2\_H AC P43356

MAG2\_HUMAN P43356;

STANDARD;

PRT;

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RESULT 11

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                                                                              Matches
                                                                                                   Query Match
Best Local
                                                                                                                                                                           Oxidoreductase; Monooxygenase; Membrane; Heme; Microso Endoplasmic reticulum; Hypothetical protein.
BINDING 455 455 HEME (BY SIMILARITY).
SEQUENCE 510 AA; 58804 MW; 6973570BF911E4E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Bioinformat:
the European Bioinformatics Institute. They
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0036778; Cyp312a1
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IGHLHIL
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Pred.
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01-NOV-1995
15-JUL-1999
                                       P57310;
O1-OCT-2000 (Rel. 40, Created)
O1-OCT-2000 (Rel. 40, Last sequence update)
O1-OCT-2000 (Rel. 40, Last annotation update)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8)
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaugler B., van den Eynde B., van der Bruggen P., Romero P., Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.; "Human gene MAGE-3 coeds for an antigen recognized on a melar autologous cytolytic T lymphocytes.";

J. Exp. Med. 179:921-930(1994).

-I- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
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DOMAIN
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MEDLINE=94102805; PubMed=8276455;
de Smet C., Lurquin C., van der E
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ACETYLMURAMOYL-L-ALANINE MURC OR BU215.
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InterPro; IPR002190; -.
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MELANOMA-ASSOCIATED ANTIGEN 2 (MAGE-2 ANTIGEN).
                                                                                                                                                                 MURC_BUCAI
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PROGRESSION. ANTIGEN RECOVER.

CYTOLYTIC T LYMPHOCYTES.

TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL 11

TISSUE SPECIFICITY: AND NECK SOURMOUS CELL CARCINOMA, L

THE AND MELANOMA, HEAD AND NECK SOURMOUS TIN NORMAL TISSUES
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                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene
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                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                    73.8%;
85.7%;
                        SYNTHETASE)
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POLY-SER.
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; 844F16335A2BECE7 CRC64;
                                                                                                                                                                   PRT;
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37;
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PARE_BORBU
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Best Local S
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Q59189;
15-DEC-1998
15-DEC-1998
15-DEC-1998
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Nature 407:81-86(2000).
-!- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).
-!- CATALTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- CATALTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE.
-!- PATHWAY: PEPTIDOGLYCAN BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
                                                                                    Utterback T., Watthey L., McDonald Garland S., Fujii C., Cotton M.D.,
                                                                                                  Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K. Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback T., Watthey L., McDonald L., Artiach P., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                          Nature
[2]
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ATCC 35210 / B31;
MEDLINE-98065943; PubMed-9403685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiotic bacterium).
Bacteria; Proteobacteria;
SEQUENCE OF
STRAIN=212;
                                                                                                                                                                                                                                                                   Borrelia burgdorferi (Lyme
                                                                                                                                                                                                                                                                                 PARE OR BB0036
                                                                                                                                                                                                                                                                                               TOPOISOMERASE
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                                                 burgdorferi
                                                                                                                                                                                                                                       NCBI_TaxID=139
                                                                                                                                                                                                                                                     Bacteria; Spirochaetales;
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                                                               "Genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                           268 IGHFYII 274
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                                                                      nd S., Fujii C.,
H.O., Venter J.
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                                      :580-586(1997).
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(Rel.
            1-83 FROM N.A
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54311 MW;
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                                                              a Lyme
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                                                                                                                                                                                                                                                                    disease spirochete).
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06359D435D5590A7 CRC64;
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                                                                                                                                                                                                                                                                                                                      update)
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                                                               spirochaete,
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(See http://www.isb-sib.ch/announce/
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57;
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                                                                 Borrelia
                                                                                                                                                                         Clayton R.A.,
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RANGE OF THE PROPERTY OF THE P

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RESULT 14
GCPE_CHLPN
ID GCPE_C
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DT 01-OCT
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OS Chlamy
OC Bacter
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Best Local S
Matches 5
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Bacter*
  pneumoniae
Nucleic Aci
                                                         MEDLINE-20150255; PubMed-10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                            Kalman S., Mitchell W., Marathe R., Lammel C., Far
Olinger L., Grimwood J., Davis R.W., Stephens R.S.
"Comparative genomes of Chlamydia pneumoniae and c
Nat. Genet. 21:385-389(1999).
                     "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia burgdorferi, B. garinii and B. afzelii.";
Microbiology 140:2931-2940(1994).

-I- FUNCTION: TOPOISOMERASE IV IS ESSENTIAL FOR CHROMOSOME
SEGREGATION. IT HAS RELAXATION OF SUPERCOILED DNA ACTIVITY.
PERRORMS THE DECATEMATION EVENTS REQUIRED DURING THE REPLIC
OF A CIRCULAR DNA MOLECULE (BY SIMILARITY).

-I- SUBBUNIT: COMPOSED OF TWO SUBBUNITS: PARC AND PARE.
                                                                                                                                                                                                                                                                                                                          MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001241; -.
Pfam; PF00204; DNA_topoisoII; 1.
PRINTS; PR00418; TPI2FAMILY.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L32861; AAC41408.1; TIGR; BB0036; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ojaimi C., Davidson B.E., Saint-Girons I., Old I.G., "Conservation of gene arrangement and an unusual organization of genes in the linear chromosomes of the Lyme disease spirochaetes Borrelia burgdorferi, B. garinii and B. afzelii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase;
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599 AA; 68774 MW; B5901F17B1CC7721 CRC64;
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28:1397-1406(2000)
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Pred. No.
1; Mismatc
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                                      Chlamydia
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В
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                                                                                                              RC STRAIN=KC583 / ATCC 35685;

RM MEDLINE=99013570; pubMed=9797224;

RA BATLISTI J.M., Smitherman L.S., Samuels D.S., Minnick M.F.;

RA BATLISTI J.M., Smitherman L.S., Samuels D.S., Minnick M.F.;

RT "Mutations in Bartonella bacilliformis gyrB confer resistance to

recommermycin Al.";

Counsermycin Al.";

L Antimicrob. Agents Chemother. 42:2906-2913(1998).

L Antimicrob. Agents Chemother. 42:2906-2913(1998).

L FUNCTION: DNA GYRASE NEGARIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-

STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE

COUNTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED

COUNTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA.

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COUNTERCONVERSION OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA

BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE

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Bacteria; Proteobacteria;
Bartonellaceae; Bartonella
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EMBL; AE002200; AAF38230.1;
EMBL; AP002246; BAA98581.1;
TIGR; CP0383; -.
SEQUENCE 613 AA; 68308 MW
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entities requires a license agreement (See )
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Nucleic Acids Res. 28:2311-2314(2000).
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Q9zdu6 homo sapien
Q9mza9 ovis aries
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Q9s1r5 streptomyce
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Pfam; PF01454; MAGE; 1.
SEQUENCE 314 AA; 34836 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9NSD3;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SOT TITIES AND DESCRICTOR COCCOCCER REPRESENTATION OF THE PROCESS 
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Q9VVF8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
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CG7692 PROTEIN.
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O1-AUG-1998 (TrE
O1-AUG-1998 (TrE
O1-MAR-2001 (TrE
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01-AUG-1998 (TIEMBLIFEL 107, Last sequence update)
01-AUG-1998 (TIEMBLIFEL 116, Last annotation update)
01-MAR-2001 (TIEMBLIFEL 116, Last annotation update)
CYTOCHROME P450 81B1 (EC 1.14.13.53) (ISOFLAVONE 2'-HYDROXYLASE).
CYP81B1 OR CYP81B1L OR CYP81B1S.
Helianthus tuberosus (Jerusalem artichoke).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyt
Magnollophyta; eudicotyledons; core eudicots; Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTIMICROBIAL COMPOUNDS OF LEGUMES.

-!- ALTERNATIVE PRODUCTS: TWO FORMS; CYP81B1L (SHOWN HERE)
CYP81B1S; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AJ000478; CAA04117.1; -.
EMBL; AJ000477; CAA04116.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Magnoliophyta; eudicotyleo euasterids II; Asterales; Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYP81B1, a plant cytochrome of fatty acids.";
J. Biol. Chem. 273:7260-7267
-i- FUNCTION: CATALYZES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Werck-Reichhart D. "Cloning, expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. BLANC COMMUN; TISSUE=TUBER, MEDLINE=98184826; PubMed=9516419;
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Trad
Pterygota; Neoptera; Endopterygota;
Ephydroidea; Drosophilidae; Drosophi
                                                                                                                                     CG7692
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Biol. Chem. 273:7260-7267(1998).

FUNCTION: CATALYZES THE HYDROXYLATION OF ISOFLAVONES, DAIDZEIN AN FORMONOMETIN, TO YIELD 2'-HYDROXYISOFLAVONES, 2'-HYDROXYDAIDZEIN, AND 2'-HYDROXYFORMONOMETIN, RESPECTIVELY (BY SIMILARITY).

CATALYTIC ACTIVITY: FORMONOMETIN + NADPH + O(2) =
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PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF LEGUMES.

ANTIMICROBIAL COMPOUNDS OF LEGUMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: ENZYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IGHLYLL
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; PS00086; CYT
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85.7%;
      Endopterygota; Diptera;
ilidae; Drosophila.
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MISSING (IN CYP81B15).
MISSING (IN CAA04116).
Y -> S (IN CAA04116).
P -> Q (IN CAA04116).
R; 38108E379BDB35C8 CRC64;
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Last sequence update)
Last annotation updat
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l; Mismatches
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                                                                    Tracheata;
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                                                                       Hexapoda; Insecta;
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                                     Brachycera; Muscomorpha;
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RL Science 287:2185-2195(2000).
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Best Local
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                                                                                                                                                            Streptomyces coelicolor Bacteria; Firmicutes; Ac
SEQUENCE FROM STRAIN-A3(2);
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                                                                                            NCBI_TaxID=1902;
                                                                                                                              Actinomycetales;
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se; FBgn0036714; CG7692.
NCE 1310 AA; 150503 MW;
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                                                                                                                                 Streptomycineae;
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BLrel. 13,
BLrel. 13,
PROTEIN.
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85.7%;
                                                                                                                                                                   Actinobacteria;
                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                               Created)
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Pred. No.
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                                                                                                                                 Streptomycetaceae; Streptomyces.
                                                                                                                                                                   Actinobacteridae;
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1.5e+02;
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                                                                                                                                                                                                                                                                                              update)
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Best Local
Matches
                           Submitted (OCT-1998) to the EMB:
-: SIMILARITY: BELONGS TO ZN-F-
EMBL; APO96371; AAC62795.1; -.
InterPro: IPR001584; -.
InterPro: IPR001878; -.
Pfam; PF00098; zf-CCHC; 1.
Pfam; PF000665; rve; 1.
PRINTS; PR00939; CCHCZNFINGER.
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01-NOV-1998 (TrE
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T2L5.9 PROTEIN.
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T2L5.9.
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082607;
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STRAIN=97000351; PubMed=8843436;
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                           STRAIN-CV. COLUMBIA;
Geisel C., Smith A.,
"The sequence of A.
                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta;
Eukaryota; viridiplantae; Embryophyta;
Magnoliophyta; eudoicotyledons; core eud
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A set of ordered cosmids and a detailed genetic at the 8 mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL; AL109972; CAB53266.1; -.
SEQUENCE 234 AA; 25619 MW; A4FEFB11CD014319 CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
Bentley S.D., Parkhill J.,
Submitted (AUG-1999) to th
 Zinc-finger.
SEQUENCE 1
                   SMART; SM00343;
                                                                                                             Waterston
                                                                                                                       STRAIN-CV.
                                                                                                                                                     Submitted
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Kinashi H., Hopwood D.A.;
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                                                                                                                       COLUMBIA;
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16,
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the EMBL/GenBank/DDBJ
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e EMBL/GenBank/DDBJ databa
                                                                                         ZN-FINGER
 M.
                                                                                         EMBL/GenBank/DDBJ databases ZN-FINGER CCHC TYPE FAMILY.
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Last sequence update)
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Pred. No.
                                                                                                                                                               T2L5.";
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C2B34A4A509B5C80
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39;
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Score

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Length 1244;

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RESULTA

QUESTION

ACCOMMENT

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       RRR RN OCC OG DET
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RX MEDLINE-20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Eviii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Coronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Coronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

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RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Copenhaver G.P., Fraser C.M., Venter J.C.,

RA Copenhaver G.P., Fraser C.M., Venter J.C.,

RA Copenhaver G.P., Fraser C.M., Venter J.C.,

RA Salzberg S.L., Fraser C.M., Venter J.C.,

RA Adams M.D., Carrera A.J., C.,

RA Adams M.D., Carrera A.J., C.,

RA Adams M.D., Carrera M.J., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adams M.D., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adams M.D., Carrera M.D., C., White O., Eisen J.A.,

RA Adam
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Best Local
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                         SEQUENCE FROM N.A. STRAIN=IF03022; MEDLINE=95206941; I
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Q45454;
01-NOV-1996
01-NOV-1998
01-NOV-1998
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OSSIM3;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE RETROELEMENT POL POLYPROTEIN.
                                                                                                                                                                                                                                                                                                            PROBABLY POSITIONED Bacillus subtilis.
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
       Meijer
                                                                                                                                                                       Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                           Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                           Plasmid pTA1060.
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Polyprotein; Zinc-finger.
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(TTEMBLrel. 01, Last sequence update)
(TTEMBLrel. 08, Last annotation update)
SITIONED IN OPERON WITH DOWNSTREAM ORF5.
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Venema G.,
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PubMed=7899081;
ma G., Bron S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.0%;
75.0%;
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2; Mismatches 0;
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                                                                                                                                                                                                           Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Q924K0;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
Q1-MAY-1999 (TREMBLrel. 10, Last annotation update)
PACTOR C PROTEIN PRECURSOR.
Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                       085748;
085748;
01-NOV-1998
01-NOV-1998
01-MAR-2001
CHEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid from Bacillus subtilis.";
Nucleic Acids Res. 23:612-619(1995).
EMBL; U32380; AAC44422.1; -.
Plasmid.
SEQUENCE 305 AA: 35577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
SEQUENCE
                                                                         CHEW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=45H;
MEDLINE=80156796; PubMed=6767606;
Biro S., Bekesi I., Vitalis S., Szabo G
"A substance effecting differentiation
"A substance and properties.";
               Treponema denticola.
Bacteria; Spirochaetales;
NCBI_TaxID=158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Purification and properties.";
Eur. J. Biochem. 103:359-363(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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NCBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and sequencing
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5; Conservative
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03943; AAC97368.1;
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                                                                                                          3 (TrEMBLrel. 08, 08) (TrEMBLrel. 08, 08)
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71.4%;
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ng of the factor C c
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                                    Spirochaetaceae; Treponema
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Last sequence update)
Last annotation updat
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Pred.
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FACTOR C PROTEIN.
; E5F57BA09D2B4EDB
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No.
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gene
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RESULT
Q9UDU6
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Best Local Similarity 100
Matches 6; Conservative
                           Pfam; PF00024; PAN; 1.
Pfam; PF00051; kringle; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRODOM; PD000583; -; 1.
PROSITE; PS00071; KRINGLE_1; UNI
PROSITE; PS00070; KRINGLE_2; 4.
                                                                                                                 InterPro; IPR000001; -.
InterPro; IPR000327; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR003014; -.
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InterPro; IPR001601; -.
InterPro; IPR002545; -.
Pfam; PF01584; CheW; 1.
Pfam; PF01799; CheW; 1.
SMART; SM00138; MeTrc; 1.
SEQUENCE 444 AA; 49706
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01-MAR-2001
HEPATOCYTE G
Hydrolase;
SEQUENCE
                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM !
                                                                                                                                                                   -!- SIMILARITY: TO SERINE PI
-!- SIMILARITY: TO CHYMOTRYI
EMBL; AC004960; AAC71655.1;
HSSP; P14210; 1BHT.
                                                                                                                                                                                                                                                        Waterston
Submitted
                                                                                                                                                                                                                                                                                                 Courtney L., Elliot G., Angell S.; "The sequence of Homo sapiens PAC clone RP5-11 Submitted (JUN-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UDU6;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greene S.R., Stamm L.V.;
"Treponema denticola chemotaxis
submitted (JUN-1998) to the EMBL
EMBL, AF074950; AAC33469.1; -.
                     SMART; SM00020; Tryp_SPc; 1.
                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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154 GHLYIL 1
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                                                                                                                                                                                                                                   SEQUENCE FROM
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STRAIN-ATCC35405;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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| (JUN-1998)
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723 AA; 82602 I
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                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                              N.A.
                                                                                                                                                                                         9) to the EMBL/GenBank/DDBJ databases
SERINE PROTEASES, TRYPSIN FAMILY.
CHYMOTRYPSIN SERINE PROTEASE FAMILY
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49706
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100.0%;
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ne EMBL/GenBank/DDBJ (
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 W.
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Pred. No.
                                          UNKNOWN_4
                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
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 627B1EF99FAD931B
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GenBank/DDBJ databases
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 CRC64;
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Query Match

78

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RESULT

Q9N996

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Matches 5
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Q9NP96;
01-OCT-2000 (TIEMBLIAL: 15, C
01-OCT-2000 (TIEMBLIAL: 15, L
01-MAR-2001 (TIEMBLIAL: 16, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                              "The harn' 2H9 gene, which is involuntially spliced gene.";
Blochim. Blochys. Acta 0:0-0(2000).
EMBL; AF13236; AAF68850.1;
EMBL; AF13250; AAF68844.1;
                                                                                                                                         Honore
"The hr
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ovis aries (Sheep).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                         "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL; AF251147; AAF87226.1; InterPro; IPR001664; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-PLACENTAL ARTERY;
Zheng J., Tsoi S.C., Magness
Zheng J., Tsoi S.C., Magness
Growth factor expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                   Biochim.
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01-OCT-2000
                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      The hnRNP 2H9 gene, which is involved
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-20461765; PubMed-10858537;
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                                interPro;
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Biophys. Acta 1492:108-119(2000)
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Last sequence update)
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Catarrhini;
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i; Hominidae;
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Best Local
Matches
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Q9NPA7;
Q1-OCT-2000
01-OCT-2000
01-MAR-2001
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                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                    "The hnRNP 2H9 gene, multiply spliced gene Biochim. Biophys. Act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-DSM 50106;
STRAIN-DSM 50106;
Bruenker P., Altenbuchner J.
Submitted (FEB-1998) to the
-1- SIMILARITY: BELONGS TO T
                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0032; HTHARAC.

PROSTIE; PS00041; HTH_ARAC_FAMILY_1; 1.

PROSTIE; PS01124; HTH_ARAC_FAMILY_2; 1.

SMART; SM00342; HTH_ARAC; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription regulation.
SEQUENCE FROM N.A
                                                                      SEQUENCE FROM N.A.
MEDLINE=20461765; PubMed=10858537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF047527; AAC34292.1; InterPro; IPR000005; -. Pfam; PF00165; HTH_AraC; 1.
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NCBI_TaxID=294;
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Bacteria; Proteobacteria;
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5; Conservative
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Primates;
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62.5%;
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                       1492:108-119(2000).
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Pred. No. 1
                                                                                                                         Craniata; Ve
Catarrhini;
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ARAC/XYLS FAMILY OF TRAN
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annotation
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i; Hominidae; Homo.
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1.3e+02;
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Search completed: June Job time: 346 sec
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=97153147; PubMed=8999868;

Mahe D., Mahl P., Gattoni R., Fischer N., Mattei M.G., Stevenin J.,

Fuchs J.P.;

"Cloning of human 2H9 heterogeneous nuclear ribonucleoproteins.

Relation with splicing and early heat shock-induced splicing arrest.";

J. Biol. Chem. 272:1827-1836(1997).
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"The hnRNP 2H9 gene, which is involved in the splicing reaction, multiply spliced gene.";
Biochim. Biophys. Acta 0:0-0(2000).
EMBL; AF132361; AAF68849.1; -.
EMBL; AF132360; AAF68847.1; -.
InterPro; IPR000504; -.
Pfam; PF00076; rrm; 2.
SEQUENCE 331 AA; 35239 MW; A3BA8D0F5FC07369 CRC64;
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Q9Y4J5,
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence update)
Q1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
RIBONUCLEOPROTEIN (HNRNP 2H9).
                                                                                                                                                                                                                                                                                                                                                                                                                     multiply spliced gene.";
Biochim. Biophys. Acta 0:0-0(2000).
EMBL; L32610; AAA5179.1; -.
EMBL; AF132360; AAF68843.1; -.
InterPro; IFR000504; -.
Pfam; PF00076; rrm; 2.
Nucleocapsid; Ribonucleoprotein.
Nucleocapsid; Ribonucleoprotein.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HONORE B.;
"The hnRNP 2H9 gene, which is involved
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                                                                                                                                                 1 RIGHLYI 7
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80 RIGHRYI 86
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85.7%; Pred. No. 1.4e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                      76.2%;
85.7%;
                               2001, 14:10:24
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                  987654321
                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB seq
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Match
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1: /SIDS6/gcgdata,
2: /SIDS6/gcgdata,
3: /SIDS6/gcgdata,
                                                                                                                                                                                                                                                                                                                                                                                                                  83.3
81.0
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Gapop 10.0 , Gapext 0.5
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42
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/SIDS6/gcgdata/geneseq/geneseqp/AA2000.DAT:
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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                Y46062
W23043
Y46263
Y47329
Y47950
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R50283
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                                                                                                                                                                                                                                                                                                SUMMARIES
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Jerusalem artichok MAGE-21 nonapeptid MAGE-21 nonapeptid Immunogenic peptid MAGE-12/HLA-B44 tu Immunogenic peptid Immunogenic peptid
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hapatocyte	leukocyte-		hepatocyté	μ.		an plas	mutant	TCF mutant having	r cytotoxi	modified	ified t	ild	TCF-II. R29819:	oinant hum				Tumour cytotoxic f	Nucleic acid trans	່"ູ	$\sim$	CLYTA-MAGE-3-His f	Lipoprotein D-MAGE	Haemagg]ntinin-Mag	ָרַע ער	GE-3 polyne	XV to X	Human MAGE-3 tumou	Baboon MAGE-3 homo	lass I	SO.	pepti	Immunogenic pentid

## ALIGNMENTS

Y05902

Jerusalem artichoke in-chain hydroxylase CYP81B1.

02-AUG-1999 (first entry)

Y05902;

Y05902 standard; Protein; 505

A

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Batard Y, Benveniste Helvig C, Le Bouquin Werck-Reichhart D;
Nucleic acid encoding plant fatty acid hydroxylases
                  WPI; 1999-264030/22.
N-PSDB; X58406.
                                                                                                                                                        Helianthus tuberosus.
                                                                                                                                                                       In-chain hydroxylase; transgenic plant; lipid; hydroxylation; oilseed; vegetable oil; crop protection; Jerusalem artichoke; CYP81B1; cytochrome P450.
                                                                        (CNRS ) CENT NAT RECH SCI.
                                                                                        06-OCT-1997;
                                                                                                        06-OCT-1998;
                                                                                                                        15-APR-1999.
                                                                                                                                        W09918224-A1.
                                                                                        97us-0060960
                                                                                                        98WO-IB01716
                                                ×Ή
                                               Cabello-Huartado
Pinot F, Salaun
                                                'n,
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Example 4; Fig 20A-B; 157pp; English

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RESULT RE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grusalem artichoke. CYPRIBL is a microsomal cytochrome P450 that CC datalyses the omega-2, omega-3 and omega-4 hydroxylation of capric, CC lauric and myristic acids. The major metabolite is the comega-3-hydroxylated compound. The invention provides isolated rucleic acids (see X58400-06) encoding plant fatty acid hydroxylases (see Y05896-902). Also claimed are host cells, transgenic plants and compositions consisting of the plant fatty acid hydroxylase, a process for isolating additional fatty acid hydroxylase, a process for isolating additional fatty acid hydroxylase in a transgenic plant, and a process of altering the fatty acid composition in a plant by expressing the plant fatty acid cydroxylase in a transgenic plant, and hydroxylating or epoxidating a fatty acid substrate in the plant. Manipulating the hydroxylated cattack by insects and other pests. The transgenic plants major action in the manufacture of e.g. lubricants, anti-slip agents, coating acents. Asternants and aurfactants.
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                           31-AUG-1992;
26-MAR-1993;
07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasticisers, coating agents, detergents and surfactants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA; histocompatability; human leucocyte antigen; probe; trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGE-21 nonapeptide
  Disclosure;
                                                                                                                                                                                                                                         Van Derbruggen
                                                                                                                                                                                                                                                                       Boon-falleur T,
                                                                                                                                                                                                                                                                                                                       (LUDW-) LUDWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
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nes 6; Conserv
                                                                        aw nona:peptide derived from tumour rejection antigen precursor presented by HLA-Al cancer cells, for use in diagnosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 IGHLYIL 8
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                                                       of.
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Page 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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93US-0037230.
93US-0073103.
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                                                       melanoma
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  33pp;
                                                          and breast cancer.
     English
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                                                                                                                                                                                                                                                                       Lurquin C,
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24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probe; treatment;
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RESULT
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Best Local S
Matches 6
antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention (see R9937-R99342), which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells (CTLs) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The peptides can also be used therapeutically to induce a CTL response to tumours (where the peptides are optionally coupled to tumour-specific antibodies), or to induce a response by CTLs that are otherwise inactive. The peptide sequences may also be used to expand specific CTLs in vitro for later return to the patient, such as for treating melanoma. Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIA binding peptide; cell lysis; cytolytic T cell; MAGE family; human; tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell; antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R99345 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involving HLA-Al subtype cancerous cells. The nucleic acid encoding the nonapeptide can be used as a probe to identify tumour cells. This sequence is homologous to the peptide described and is encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              An isolated nonapeptide having the amino acid sequence Glu-Val-Asp-pro-Ile-Gly-His-Leu-Tyr is derived from the tumour rejection antigen precursor encoded by the MAGE-3 gene and presented by HLA-Al. The nonapeptide can be used in a vaccine to treat a cancerous condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGE-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R99345
                                                                                                                                                                                                                                 New nona:peptide(s) that bind
by specific cytolytic T cells,
tumours and to expand T cells
                                                                                                                                                                                                                                                                                                 WPI; 1996-402317/40.
N-PSDB; T35410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09626214-A1
                                                                                                                                                                                                      Example 4; Fig 4; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                        (LUDW-) LUDWIG INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                       23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                             Romero
                                                                                                                                                                                                                                                                                                                                                             Boon-Falleur T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RIGHLY 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is sequence is homologous the MAGE-21 gene.
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                         in vitro.
                                                                                                                                                                                                                                                    to HLA molecule(s), for diagnosis and
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Den Eynde B,
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BB
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Van Der Bruggen
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CC v45390 to y48214 represent specifically claimed immunogenic peptides CC having a human major histocompatibility complex (MHC) Class I (also CK hown as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-2.1, Al, Al. 2 or All. 1 or HLA-B or C) and induce a cytotoxic T cell Cresponse against the antigen from which the peptide is derived. CC control of I lymphocytes (CTLS) which destroy antigen-bearing cells are CC normally induced by an antigen in the form of a peptide fragment bound CC normally important in tumour rejection and in fighting viral CC are particularly important in tumour rejection and in fighting viral CC infections. The peptides are therefore useful therapeutically to treat CC or prevent viral infections and cancers in mammals (especially humans) CC prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in CC cancer, or used to treat chronic or acute conditions. They are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells can be identified by using DNA encoding the nonapeptides as probe Non-human cells transformed with the HLA-Al gene and a DNA sequence encoding one of the peptides, can be used to generate CTLs, or to detect the presence of CTLs in human samples. The non-human transformed cells when polytransformed, are universal effector cells, and can be used in vaccines, or for treating melanoma or breast cancer.
                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cance prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                  Claim 1; Page 54; 150pp; English
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4 righly 9
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                                                                                                                                                                                                                                                                                                                     with HLA binding motif, and viral diseases
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Pred. No.
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3.2e+05;
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                                    This peptide is a tumour rejection antigen presented by a HLA-B44 complexed and derived from a MAGE-12 tumour rejection antigen (WR2038443). Consider tumour rejection antigens (WR2038443). Consider the bind to HLA-B44 positive cells, making them useful in identifying cells which present HLA-B44 molecules on their surfaces for use in the diagnosis and therapy of cellular abnormalities. The complex of the tumour rejection antigen and HLA consequence of tumour rejection antigens, or complexes of tumour rejection antigens and that HLA-B44, can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigen/HLA complexes on their surface, such as non-proliferative cancer cells and non-proliferative
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Best Local :
                                                                                                                                                                                                                                                                 Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
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                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAGE-12; tumour rejection antigen precursor; TRAP; HLA-B44; human leukocyte antigen B44; cytotoxic T lymphocyte; cancer
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                         as non-proliferative transfectants.
                                                                                                                                                                                                                                          Claim
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                                                                                                                                                                                                                                         Page 51; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy;
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5. 3.2e+05;
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                         CC having a human major histocompatibility complex (MHC) Class I (also CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell Cresponse against the antigen from which the peptide is derived. CC cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are commally induced by an antigen in the form of a peptide fragment bound CC to a HLA molecule, rather than the intact foreign antigen itself, and CC are particularly important in tumour rejection and in fighting viral cifections. The peptides are therefore useful therapeutically to treat CC infections. The peptides are therefore useful therapeutically humans) CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. CC individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also cuseful diagnostically, and can be used to induce a cytotoxic T cell composure contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The coll contacting the immunogenic peptides are also useful therapeutically and for immunisation as above.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 64; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               and diagnosis of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide having a human leukocyte antigen binding motif #874.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.0%; Score 34;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                and viral diseases
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0.56;
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Best Local S
Matches 6
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                                                                                        are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to
                                                                                                                                                                                                                                                 Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and to a HLA molecule, rather than the intact foreign antigen itself, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
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                                 response, by contacting a cytotoxic T cell with the peptide e.g. produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                 CC Y45390 to Y48214 represent specifically claimed immunogenic peptides CC CC having a human major histocompatibility complex (MHC) Class I (also CK nown as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CF HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell cresponse against the antigen from which the peptide is derived. CC Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound CC to a HLA molecule, rather than the intact foreign antigen itself, and CC are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat correct or prevent viral infections and cancers in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. CC Individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also cuseful diagnostically, and can be used to induce a cytotoxic T cell cresponse, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The cC produce CTLs ex vivo for infusion back into a patient. The cC therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1;
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                                              CC v45390 to v48214 represent specifically claimed immunogenic peptides CC having a human major histocompatibility complex (MHC) Class I (also CK known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytocoxic T cell CC response against the antigen from which the peptide is derived. CC Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are CC normally induced by an antigen in the form of a peptide fragment bound CC an HLA molecule, rather than the intact foreign antigen itself, and CC are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat CC or prevent viral infections and canners in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. CC They can be administered as vaccines to elicit an immune response in CC individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also CC useful diagnostically, and can be used to induce a cytotoxic T cell CC response, by contacting a cytotoxic T cell with the peptide e.g. to CC produce CTLs ex vivo for infusion back into a patient. The CC polyucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also
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                                CC having a human major histocompatibility complex (MHC) Class I (also CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell Cryotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are commally induced by an antigen in the form of a peptide is derived. CC crotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are commally induced by an antigen in the form of a peptide irragment bound CC to a HLA molecule, rather than the intact foreign antigen thound CC are particularly important in tumour rejection and in fighting viral CC infections. The peptides are therefore useful therapeutically to treat CC or prevent viral infections and cancers in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also useful diagnostically and can be used to induce a cytotoxic T cell cresponse, by contacting a cytotoxic T cell with the peptide e.g. to CC produce CTLs ex vivo for infusion back into a patient. The CC therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                            CC vat5390 to v48214 represent specifically claimed immunogenic peptides CC having a human major histocompatibility complex (MHC) Class I (also CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell C response against the antigen from which the peptide is derived. CC Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are constaintly induced by an antigen in the form of a peptide fragment bound CC to a HLA molecule, rather than the intact foreign antigen itself, and care particularly important in tumour rejection and in fighting viral confections. The peptides are therefore useful therapeutically to treat cor prevent viral infections and cancers in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C. AIDS, and renal carcinoma. CC They can be administered as vaccines to elicit an immune response in C individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also cuseful diagnostically, and can be used to induce a cytotoxic T cell C response, by contacting a cytotoxic T cell with the peptide e.g. to CC produce CTLs ex vivo for infusion back into a patient. The cc therapeutically and for immunisation as above.
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Y48011
                          CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes (HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell CC response against the antigen from which the peptide is derived. CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound CC to a HLA molecule, rather than the intact foreign antigen itself, and CC are particularly important in tumour rejection and in fighting viral CC infections. The peptides are therefore useful therapeutically to treat C or prevent viral infections and cancers in mammals (especially humans) CC e.g. prostate cancer, hepatitis B and C, ALDS, and renal carcinoma. CC They can be administered as vaccines to elicit an immune response in CC individuals susceptible or otherwise at risk of viral infection or CC cancer, or used to treat chronic or acute conditions. They are also CC response, by contacting a cytotoxic T cell with the peptide e.g. to CC produce CTLs ex vivo for infusion back into a patient. The CC custometrically and for immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                          Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 132; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-551214/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide having a human leukocyte antigen binding motif #2622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwood
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RESULT
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  RESULT
Y98994
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                                                                                                                                                                                                                                                                                                                        B08827-37 represent melanoma associated antigen (MAGE)-3 derived immunogenic peptides. The peptides are capable of binding to major histocompatibility complex (MHC) class II molecules. Stimulation with the peptides induces proliferation of CD4+ T cells, and of their cytolytic activity. CD4+ T cells exposed to the peptides were able to cause lysis of melanoma cells expression MAGE-3 and HLA-DR molecules. The peptides are useful for inducing an immune response against tumour cells expressing a MAGE-3 antigen. They are also useful for the preparation of anti-tumour medicament for use as a vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Melanoma associated antigen-3; MAGE-3; immunogenic peptide; major histocompatibility complex; MHC; class II molecule; tumour; CD4+ T cell proliferation; melanoma cell; immune response; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful
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Mllograft
           immune response; chronic viral disease; cancer; autoimmune dirheumatoid arthritis; multiple sclerosis; myasthenia gravis;
                     Human leucocyte antigen; HLA class II; antigen epitope; pharmaceuti immune response; chronic viral disease; cancer; autoimmune disease;
                                                            HLA class
                                                                                   07-AUG-2000
                                                                                                            Y98994;
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                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 18;
rejection;
                                                         II binding antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine
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                                                                                                                                 Peptide;
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allergy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
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                                                           epitope peptide #183
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lyme disease; hepatitis;
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prostate cancer,
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College Proposition and the period of the world wide population. The class DR molecules, representative of the world wide population. The class DR molecules, representative of the world wide population. The competition or equal to 1,000 nM. The pharmaceutical can be used to induce a content of the content of diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia content of content of the content of diseases that can be content of the content of diseases that can be content of content of the content of content of the content of content of diseases and could herefore be used in cases of content of viral diseases and content. Examples of diseases that can be content of content of content of diseases that can be content of content o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 43;
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                                                                                   Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from those represented by peptides
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                                                                                 Score 33; DB; Pred. No. 1.4
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tides Y98812-Y99339
human leucocyte anti
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    ROHZ_HUMAN
C312_DROME
FEGU_HCMVA
LEU3_THIFE
CD51_THIFE
ARE_BORBU
AT1D_HUMAN
AT1D_HUMAN
AT1D_HUMAN
Y077_HAEIN
Y077_HAEIN
PQOB_ACICA
PAGE_HUMAN
PQOB_ACICA
RAG6_HUMAN
TG1_ARCPU
SYH_METJA
                                                                                                                                                                                                                                                                                                                                                                                                        MAGC_HUMAN
GCPE_CHLPN
GYRB_BARBA
HGF_HUMAN
HGF_HUMAN
HGF_HUMAN
MGCAR_XENIA
TIPA_PHAVU
SNC1_HUMAN
CDS1_ARATH
ROH1_HUMAN
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p14210 homo sapien Q08048 mus musculu p17945 rattus norv p43356 homo sapien p43357 homo sapien p43357 homo sapien p43358 phaseolus v Q16533 homo sapien p52597 homo sapien p52597 homo sapien p5795 homo sapien p5795 homo sapien p5796 drosophila p16785 human cytom Q56268 thiobacilu Q04940 sphosphati Q26346 methanobact p57310 buchnera ap p39965 saccharomyc Q59189 borrelia bu p98198 homo sapien Q52271 rickettsia p77941 rickettsia p77941 rickettsia p77941 rickettsia p77941 rickettsia p77979 acinetobact p43356 homo sapien Q82787 archaegylob Q58787 archaegylob Q58787 archaegylob Q58787 archaegylob Q58787 archaegylob Q58406 methanococc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43365 homo sapien
Q9z8h0 chlamydia p
P94281 bartonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
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45	44	43	42	41	40	39	38	37	36	35	34
29	29	29	29	30	30	30	30	30	30	30	30
63.0	63.0	63.0	63.0	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2
230	193	167	76	3988	3898	906	883	683	551	510	459
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VME1_CVHOC	NADD_BORBU	LSPA_CHLTR	RPON_ARCFU	POLG_BVDVN	POLG_BVDVS	RPOL_BPK11	RPOL_BPT7	EFGL_THEMA	CC14_YEAST	C933_SOYBN	NEK3_HUMAN
Q01455 human coron	O51723 borrelia bu	084413 chlamydia t	029135 archaeoglob	P19711 bovine vira	Q01499 bovine vira	P18147 bacteriopha	P00573 bacteriopha	Q9x1y4 thermotoga	Q00684 saccharomyc		P51956 homo sapien

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G.,
Eisen J., Fraser C.M.,
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation updat
GCPE PROTEIN HOMOLOG.
GCPE OR CPN0373 OR CP0383
                                                                                                                                                                                     EMBL; AE001621; AAD18517.1;
EMBL; AE002200; AAF38230.1;
EMBL; AP002546; BAA98581.1;
TIGR; CP0383; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grinwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
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Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
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    -!- SIMILARITY: BELONGS TO THE GCPE FAMILY.

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1 VRIGHLYI 8
                                                             Similarity 7; Conserv
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9; Conser
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                                                                                                                                                                 68308 MW;
                                                                                76.1%;
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                                                           Score 35; DB Pred. No. 17; 1; Mismatches
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Pred. No. 0.0
); Mismatches
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17;
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y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
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GYRB_BARBA
ID GYRB_B
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RESULT 4
HGF_HUMAN
ID HGF_HUMAN
AC P14210;
DT 01-JAN-1990 01-JAN-1991 01-AUG-1991
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15-DEC-1998 (Rel. 37,
01-OCT-2000 (Rel. 40,
DNA GYRASE SUBUNIT B (
                                                                                                                                                                                                                                                                                                                                                                          Topoisomerase; Isomerase; ATP-binding; Antibiotic resistance. VARIANT 124 124 G -> S (IN COUMERMYCIN A1 MUTANT). VARIANT 184 184 R -> Q (IN COUMERMYCIN A1 MUTANT). VARIANT 214 214 T -> A (IN COUMERMYCIN A1 MUTANT). VARIANT 214 214 T -> I (IN COUMERMYCIN A1 MUTANT). SEQUENCE 692 AA; 77445 MW; F54948EEF342281F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bartonella bacilliformis.
Bacteria; Proteobacteria; alpha subdivision;
Bartonellaceae; Bartonella.
NCBI_TaxID=774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001241;
InterPro; IPR002288;
Pfam; PF00986; DNA_gyraseB_C; 1.
Pfam; PF00204; DNA_topoisoII; 1.
PRINTS; PR00418; TPIZFAMILY.
PROSITE; PS00177; TOPOISOMERASE_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99013570; PubMed=9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U82225; AAC71079.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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    13,
19,
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HEPATOCYTE GROWTH F. (HEPATOCOETTIN A).
HGF OR HPTA.
HOMO
MUTAGENESIS.
MUTAGENESIS.
MEDLINE=92331602; PubMed=1321034;
Lokker N.A., Mark M.R., Luis E.A.
Lokker J.B., Godowski P.J.;
                                                                                                                                                native an Biochem. [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-91340155; PubMed-1831432;

MEDLINE-91340155; PubMed-1831432;

Seki T., Hagiya M., Shimonishi M., Nak

"Organization of the human hepatocyte
Gene 102:213-219(1991).
                                                                                                                                                                                                                                                                                                                                                                 Nature
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; )
                                                                                                                                                                                                                                                                                                                  TISSUE=Embryonic f
MEDLINE=91334393;
Weidner K.M., Arak
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90066676; pubMed-2531289;
Nakamura T., Nishizawa T., Hagiya M.
Sugimura A., Tashiro K., Shimizu S.;
"Molecular cloning and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth factor from human leukocyte.";
Biochem. Biophys. Res. Commun. 172:321-327(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seki T., Ihara I., Sugimura A., Shimonishi M., N
Asami O., Hagiya M., Nakamura T., Shimizu S.;
"Isolation and expression of cDNA for different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89392017; PubMed-2528952; Miyazawa K., Tsubouchi H., Naka D., Arakaki N., Nakayama H., Hirono S.,
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SEQUENCE FROM N.A.
TISSUE=Placenta;
                                                                Biochem.
                                                                                                            MEDLINE-93129192; Put
Shimizu N., Hara H.,
                                                                                                                     CARBOHYDRATE-LINKAGE SITE 476.
MEDLINE=93129192; PubMed=1482348;
                                                                                                                                                                                        Yoshiyama Y., Arakakai N., Naka
Nakayama H., Gohda E., Kitamura
Hishida T., Daikuhara Y.;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Leukocyte;
MEDLINE=91025062; PubMed=2145836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys.
                                                                                                   Nakamura
                                                                                                                                                                  "Identification of the N-terminal residue of the heavy chain native and recombinant human hepatocyte growth factor.";
                                                                                                                                                                                                                           MEDLINE-91207365;
                                                                                                                                                                                                                                                                      hepatocyte
                                                                                                                                                                                                                                                                                             Birchmeier
                                                                                                                                                                                                                                                                                                          Rieder
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular cloning and sequence analysis of cDNA growth factor.";
                                                                                      "Hepatocyte growth
                                                                                                                                                                                                                                                                                   "Evidence for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E., Daikuhara Y.,
                                                                                                                                                                                                                                                                                                       H., Fonatsch
                                                                            alpha
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                    -91334393; PubMed=1831266;
K.M., Arakaki N., Hartmann G.,
H., Fonatsch C., Tsubouchi H., J
                                                                 Biophys.
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iophys. Res.
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S.;
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Commun. 175:660-667(1991).
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/te growth factor~encoding gene.";
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X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.

MEDLINE-99036858; PubMed-9817840;

Olltsch M., Lokker N.A., Godowski P.J., de Vos A.M.;

"Crystal structure of the NK1 fragment of human hepatoc;
factor at 2.0-A resolution.";

Structure 6:1383-1393(1998):

-i- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCI
HEPATOCYTE CELLS, SEEMS TO BE AN HEDATOTROPHIC FACTO
AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES ANI
IT HAS NO DETECTABLE PROTEASE ACTIVITY.

-I- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN L.
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SIMILARITY: BELONGS TO PEPTIDASE FAMIL-
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human hepatocyte growth
http://www.isb-sib.ch/announce/
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EMBL; D90334; BAA14348.1; JOINED.

InterPro; IPR000 InterPro; IPR001 InterPro; IPR001 InterPro; IPR001 InterPro; IPR002 Pfam; PF00024; L Pfam; PF00089; t EMBL; L; M73239; AAA642 L; M73240; AAA642 J10579; J10579; S06794; S06794 2HGF; 24-JUN-98 1BHT; 18-NOV-98 142409; D90328; D90329; D90330; D90334; D90318; D90319; D90333: D90332; D90324; D90322; D90320; S01.976; teDB; IPR000001; -. IPR001254; -. IPR001314; -. IPR003014; -. 24-JUN-98. BAA14348.
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PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein;
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Mammalia; E
               TISSUE-Mammary fibroblast;
MEDLINE-94183257; PubMed-8135822;
Sasaki M., Nishio M., Sasaki T., Enami J.;
Sasaki M., Nishio M., Sasaki T., Enami J.;
Fidentification of mouse mammary fibroblast-derived factor as hepatocyte growth factor. 773-770/1004)
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MEDLINE-94060105; PubMed-8241272;
Liu Y., Michalopoulos G.K., Zarne
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Lee C.C., Kozak C
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ALTERNATIVE PRODUCTS: A SH
ALTERNATIVE RNA SPLICING.
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CHIN. BIOPHYS. ACTA 1216:299-303(1993).

FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HERATCOCYTE CELLS, SEEMS TO BE AN HERATCOTROPHIC FACTOR, AN AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL IT HAS NO DETECTABLE PROTEASE ACTIVITY.

SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED
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Kozak C.A., Yamada K.M.;
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equires a license agreement (S email to license@isb-sib.ch).
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PRINTS; PRO00722; CHYMOTRYPSIN.

PROSITE; PS00021; KRINGLE\_1; 4.

PROSITE; PS50070; KRINGLE\_2; 4.

Growth factor; Kringle; Glycoprotein; BAA01064.1; BAA01065.1; AAB31855.1; CAA51054.1; ALT\_INIT. (See http://www.isb-sib.ch/announce/ Serine protease homolog; collaboration -Loutstation -

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128 207 289 384 470 728 728 85 607 295 403

KRINGLE 1.

KRINGLE 2.

KRINGLE 3.

KRINGLE 4.

SERINE PROTEASE-LIKE.

SERINE PROTEASE-LIKE.

BY SIMILARITY.

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HEPATOCYTE GROWTH FACTOR ALPHA CHAIN
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A Okajima A., Miyazawa K., Kitamura N.;

A Okajima A., Miyazawa K., Kitamura N.;

Primary structure of rat hepatocyte growth factor and induction of its mrNA during liver regeneration following hepatic injury.";

Leur. J. Blochem. 193:375-381(1990).

C -: FUNCTION. HGF IS A POTENT MITOCEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS AS GROWTH FACTOR FOR A BROAD SPECTROM OF TISSUES AND CELL TYPES.

AS GROWTH FACTOR FOR A BROAD SPECTROM OF TISSUES AND CELL TYPES.

C IT HAS NO DETECTABLE PROTEASE ACTIVITY.

C -: SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A DISULFIDE BOND.

C -: SIMILARITY: DELONGS TO PEPTIDASE FAMILY SI; ALSO KNOWN AS THE STANDARD CONTAINS 4 KRINGLE REGIONS.
                                     EMBL; D90102; BAA14133.1; -
EMBL; X54400; CAA38266.1; -
PIR; S13211; S13211.
PIR; A35644; A35644.
HSSP; P14210; 2HGF.
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
(HEPATOPOEITIN A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HGF_RAT
P17945;
                                                                                                                                                                                                   between the Swiss Institute of Bioinformat. the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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STRAIN-WISTAR; TISSUE-Liver;
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Mammalia; Eutheria;
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Rattus norvegicus (Rat).
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                                                                                                                                                              s requires a license agreement (See an email to license@isb-sib.ch).
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S., Nakamura T.;
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Sciurognathi; Muridae;
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE
PRINTS; PR00722; CHYMOTRYPSIN
PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
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               Gaugler B., van den Eynde B., van der Brugaforio J.J., de Plaen E., Lethe B., Bras "Human gene MAGE-3 codes for an antigen I autologous cytolytic T lymphocytes."; J. Exp. Med. 179:921-930(1994).
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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MEDLINE-94102805; PubMed-8276455;
de Smet C., Lurquin C., van der B
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etazoa; Chordata;
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"Cloning and analysis of MAGE-1-related genes.";
Biochem. Biophys. Res. Commun. 202:549-555(1994).
-I- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGO CYTOLYTIC T LYMPHOCYTES.
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Gaforio J.J., de Plaen E., Lethe B., Brasseur F., I
"Human gene MAGE-3 codes for an antigen recognized
autologous cytolytic T lymphocytes.";
Exp. Med. 179:921-930(1994).
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Eukaryota; Metazoa; Chordata;
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170
V->D: IMPROV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L18920; AAA17729.1; -. MIM; 300173; -.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94157413; PubMed=8113684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAGEA3 OR MAGE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                  MEDLINE=94311935; PubMed=8037761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VRIGHLYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS CYTOLYTIC T LYMPHOCYTES.
TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES.
   TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES, SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCIXOMA, LUNG CARCIXOMA, AND BEAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT FOR TESTES AND PLACENTA. NEVER EXPRESSED IN KIDNEY TUMORS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WITH MAGE-12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VPISHLYIL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01454; MAGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35055 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71
77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB Pred. No. 21; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V->D: IMPROVES ABILITY TO BIND; 844F16335A2BECE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Length 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ANTIGEN MZ2-D).
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Boon T.;
d on a melanoma
                                                                                                                                                       AUTOLOGOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO HLA-A1
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RESULT 9
GCKR_XENLA
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCKR_XENLA
Q91754;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
MUTAGEN
                         InterPro; IPR001347;
InterPro; IPR001741;
Pfam; PF01380; SIS; 1
                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                             Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen E.; "Cloning and expression of a Xenopus liver cDNA encoding a fructose-phosphate-insensitive regulatory protein of glucokinase."; Eur. J. Biochem. 225:43-51(1994).

-i- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COMPLEX WITH
                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=95010134; PubMed=7925465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; Multigene family; Tumor antigen.
DOMAIN 40 43 POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U03735; AAA17446.1;
               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                             EMBL; X80901; CAA56863.1;
                                                                                                                                                                                                                                    <u>-</u>
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01454; MAGE;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 IGHLYI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 IGHLYI 8
                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEUKEMIAS AND LYMPHOMAS.
SIMILARITY: BELONGS TO THE MAGE FAMILY.
                                                                                                                                                                                                                                                   THIS ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
               PS01272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 35, Created)
(Rel. 35, Last sequence up
(Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170
176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
GCKR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170
176
34747
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100.0%;
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 WW.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D->A: ABOLISHES HLA-A1 BINDING Y->A: ABOLISHES HLA-A1 BINDING; 3F5EB13D1C9946A1 CRC64;
 41B72C1981D1BA52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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21;
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71.7%;

Score

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DB 1;

Length 619;

Best Matches

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Similarity 6; Conser

llarity 100 Conservative

J.08; 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN.";
Plant Physiol. 100:1787-1795(1992).
Plant Physiol. CHANNEL PROTEIN IN TONOPLAST. THESE PROTEINS MAY ALITHED PROTEIN. CHANNEL PROTEIN IN TONOPLAST. THE DIFFUSION OF AMINO ACIDS AND/OR PEPTIDES FROM THE TONOPLAST.
INTERIOR TO THE CYTOPLASM.
-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: FOUND IN ALL SEED TISSUES THAT ARE ALIVE SEED MATURITY, BUT NOT IN TISSUES THAT LOSE VIABILITY DURING SEED MATURITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPA_PHAVU STANDARD; PRT; 256 AA.

P23958;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 22, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP).
Phaseolus vulgaris (Kidney bean) (French bean).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papillionoideae; Phaseolus.
                                                                                                                                      TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
the Euro
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"An intrinsic tonoplast protein of protein storage vacuoles is structurally related to a bacterial solute transporter (claim to call 2:525-532(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 11-21.
STRAIN-CV. GREENSLEEVES; TISSUE-Seed;
MEDLINE-93044491; PubMed-2152174;
                                                          TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               PIR; JQ1106; JQ1106.
PIR; S26742; S26742.
InterPro; IPR000425;
                                                                                                                                                                                                                                                                                                                         PRINTS; PR00783; MINTRINSICP. PROSITE; PS00221; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X62873; CAA44669.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson K.D., Chrispeels M.J.; "Tonoplast-bound protein kinase phosphorylates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHORYLATION BY CDPK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3885;
                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00230; MIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE TRANSMEMBRANE CHANNEL MIP FAMILY
           DOMAIN
                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                             Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327
                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GHLYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: PHOSPHORYLATED BY A TONOPLAST-BOUND CALCIUM-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHLYIL
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           25
45
58
78
103
122
144
165
170
                                                                                                                                                                                                                                                                                               ransmembrane;
           24
44
47
77
102
121
143
164
169
189
                                                                                                                                                                                                                                                                 Multigene family; Seed; Pho
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
VACUOLAR (POTENTIAL).
                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
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VACUOLAR (POTENTIAL).
                                                                                                             VACUOLAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TONOPLAST. THESE PROTEINS MAY ALLOW
                                                                                                                                                                                                                                                                                          Seed; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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Query Match Best Local S Matches 5

Similarity 5; Conser

Conservative

69.68; 55.68;

Score 32; Pred. No.

DВ 39;

1;

Length 368 Indels

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Gaps

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Query Match
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Matches 5
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DOMAIN
MOD_RES
SEQUENCE
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Q16533;
                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
SURINA ACTIVATING PROTEIN COMPLEX 43 KDA SUBUNIT (SNAPC 43 KDA SUBUNIT) (PROXIMAL SEQUENCE ELEMENT-BINDING TRANSCRIPTION FACTOR SUBUNIT) (PSE-BINDING FACTOR GAMMA SUBUNIT) (PTF GAMMA SUBUNIT).
                                                   EMBL; Z47542; CAA87590.1;
EMBL; U44754; AAC50358.1;
MIM; 600591:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outsit the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for containing the content is the condition of the content is not removed.
             Transcription regulation. DOMAIN 347 352
                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE~96104548; PubMed~8524284; Yoon J.B., Roeder R.G.;
                                                                                                                                                                                                                                                                                                                                                                                                  RNA polymerase II and III Nature 374:653-656(1995).
                                                                                                                                                                                                                                                                                                                                                                                                            Henry R.W., Sadowski C.L., Kobayashi R., Hernandez N.; "A TBP-TAF complex required for transcription of human RNA polymerase II and III.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE MEDLINE=95231630; PubMed=7715707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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  SEQUENCE
                                        TRANSFAC; T01680;
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CYTOPLASMIC (POTENTIAL).

PHOSPHORYLATION (BY CDPK) (PROBABLE).

7862A0AC8EB46810 CRC64;
 POLY-GLU.
; 324E89CF8B540C32 CRC64;
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Honore B., Rasmussen H.H., Vorum H., Dejgaard K., Liu X.,
Gromov P., Madsen P., Gesser B. Tommerup N., Celis J.E.;
"Heterogeneous nuclear ribonucleoproteins H, H', and F are members of
a ubiquitously expressed subfamily of related but distinct proteins
encoded by genes mapping to different chromosomes."
J. Biol. Chem. 270:28780-28789(1995).
-i- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR
RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE
FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING
FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. PROBABLY BINDS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
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01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last seq
01-0CT-2000 (Rel. 40, Last ann
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Aarhus/Ghent-2DPAGE;
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Homo sapiens (Human).
Homo sapiens (Human).
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SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
   RIGHLYI 8
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                                                                                                                                                          00076; rlm, ...

PS50102; RRM, RNP_1; FALSE_NEG.
PS00030; RRM_RNP_1; FALSE_NEG.

Protein; RNA-Binding; Ribonucleoprotein; Repeat.

RNA-BINDING (RRM) 1.

11 188 RNA-BINDING (RRM) 2.

289 366 RNA-BINDING (RRM) 3.

A5672 MW; D14E170631FB1F31 CRC64;
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Rel. 40, Last annotation update)
NUCLEAR RIBONUCLEOPROTEIN F (HNRNP
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CDS1_ARATH
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-i-FUNCTION: MAY BE INVOLVED IN THE SYNTHESIS OF MINOR PHOSPHOLIPIDS AND IN MODULATION OF IP3-MEDIATED SIGNAL TRANSDUCTION.
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004928; 048808;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
11-OCT 2000 (Rel. 40, Last annotation update)
PHOSPHATIDATE CYTIDYLLYLFRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIGLYCEROL SYNTHASE) (CDS) (CTP-PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) (CDP-DAG SYNTHETASE).
CDS1 OR F2401.17.
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                                                                                                                           TRANSMEM
TRANSMEM
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Kopka J., Ludewig M., Mueller-Roeber B.;
"Complementary DNAs encoding eukaryotic-type cytidine-5'-diphosphate-
diacyjglycerol synthases of two plant species.";
Plant Physiol. 113:997-1002(1997).
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STRAIN=CV. C24; TISSUE=Flower,
                                                             TRANSMEM
                                                                                                                                                                                         Transmembrane
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                                                                                                                                                                                                                                                 PROSITE; PS01315;
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PROSITE; PS01315; CDS; 1.
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SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
SIMILARITY: BELONGS TO THE CDS FAMILY.
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   421 AA;
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149
206
246
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226
266
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Ouery Match 69.
Best Local Similarity 75.
Matches 6; Conservative

69.6%;

Score 32; DB Pred. No. 45; 1; Mismatches

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Pfam; Processor of the Pfam; 3.
Pfam; Posson of the Processor of the Proce
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MEDLINB-94203790; PubMed-7512260;
Matunis M.J., Xing J., Dreyfuss G.;
"The hnRNP F protein: unique primary structure,
"The properties, and subcellular localization.";
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Aarhus/Ghent-2DPAGE: 4429;
Aarhus/Ghent-2DPAGE: 5416;
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Homo sapiens (Human).
Homo sapiens (Human).
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01-OCT-2000
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P31943;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L22009; AAA91346.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rasmussen H.H., van Damme Vandekerckhove J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Keratinocytes;
MEDLINE-93162043; PubMed-1286667;
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                                                                                                                                                                                                 InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 200-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN (HRNNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG). SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.

**TISSUE SPECIFICITY: EXPRESSED UBIODITOUSLY.

**DOMAIN: BACH QUASI-RRM REPEAT BOUND POLY(RG), WHILE ONLY THE N-TERMINAL QRAM BOUND POLY(RC) AND POLY (RU). NONE OF THE REPEATS BOUND DETECTABLE AMOUNTS OF POLY(RA).

**SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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                                                                                                                                                                                                                                                    601035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acids Res.
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Rasmussen H.H., Vorum H., Dejgaard K.,
Tommerup N., Cel:
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(Rel. 34, Last seq
(Rel. 40, Last ann
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Rel. 40, Last annotation update)
NUCLEAR RIBONUCLEOPROTEIN H (HNRNP
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                                                      Ribonucleoprotein; Repeat.
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RA GLOMOV P., Madsen P., Gesser B., Tommerup N., Cells J.E.;
RT "Heterogeneous nuclear ribonucleoproteins H, H', and F are members of
RT a ubiquitously expressed subfamily of related but distinct proteins
RT encoded by genes mapping to different chromosomes.";
RL J. Biol. Chem. 270:28780-28789(1995)
C.-: FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR
C.-: RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHICH PROVIDE THE SUBSTRATE
C. FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO BEFORE BECOMING
CC. FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG).
C. C. SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
C. C. SUBCELLULAR LOCATION: NUCLEAR; NUCLEOPLASM.
C. SUBCELLULAR LOCATION: EXPRESSED UBIQUITOUSLY.
C. SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
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1-OCT-2000 (Rel. 40
HETEROGENOUS NITT
HNRPH2 OR FTT
YOMO SAT
                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isbsorsend an email to license@isbsbbch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vorechovsky I., Vetrie D., Holland J., Bentley D.R., Thomas K., Zhou J.N., Notarangelo L.D., Plebani A., Fontan G., Ochs H.D.; "Isolation of cosmid and cDNA clones in the region surrounding the BTK gene at Xg21.3-q22."; Genomics 21:517-524(1994).
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P55795;
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Oeltjen J.C., Liu X., Lu J., Malley T.M., Allen R.C.,
Belmont J.W., Gibbs R.A.;
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Rel. 40, Last annotation update)
NUCLEAR RIBONUCLEOPROTEIN H' (HNRNP H') (FTP-3).
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Primates;
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RNA-BINDING (RRM) 2.
RNA-BINDING (RRM) 3.
2 X 16 AA GLY-RICH APPROXIMATE REPEATS.
1-1.
1-2.
2 X 19 AA PERFECT REPEATS.
2-1.
2-2.
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Pred. No. 48;
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DR AARDAS/GHENT-2DPAGE; 4432; IEF.

DR AARTHUS/GHENT-2DPAGE; 4432; IEF.

DR MIM; 601036; ---

DR InterPro; IPRO00504; ---

DR PROSTIE; PS00030; RRM; 3.

DR PROSTIE; PS00030; RRM; ARP_1; FALSE_NEG.

PROSTIE; PS00030; RRM_RNP_1; FALSE_NEG.

PROSTIE; PS00030; RRM_RNP_1; FALSE_NEG.

PROSTIE; PS00030; RRM_RNP_1; FALSE_NEG.

PROMAIN 111 188 RNA-BINDING (RRM) 1.

PT DOMAIN 234 439 2 X 10 AN BINDING (RRM) 3.

PT DOMAIN 234 439 1-1.

PT DOMAIN 354 372 2-1.

PT REPEAT 354 392 2 X 19 AN PERFECT REPEATS.

PT REPEAT 374 392 2-1.

PREPEAT 375 AND PERFECT REPEATS.

PREPEAT 374 392 2-1.

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Copyright (c) 1993 - 2000 Compugen Ltd.
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O9rmz0 bacillus an O9vxf8 drosophila O49122 methylobact O9vxf8 buchnera ap 006769 mycobacteri O9udu6 homo sapien O82607 arabidopsis O28287 archaeoglob O9z4k0 streptomyce O9yfk2 aeropyrum p O9uwx3 sulfolobus O49639 arabidopsis O49639 arabidopsis
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Q1-OCT-2000 (TrEMBLrel. 15, C:
Q1-OCT-2000 (TrEMBLrel. 15, L:
Q1-MAR-2001 (TrEMBLrel. 16, L:
MELANOMA ANTICEN FAMILY A12.
MAGEA12.
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EMBL; U82671; AAF44789.1; -.

InterPro; IPR002190; -.

Pfam; PF01454; MAGE; 1.

SEQUENCE 314 AA; 34836 MW
                                                                                                                                                                                                                               Mailon A.M., Platzer M., Bates R., Gloeckner G., Botcherby M., Mordsiek G., Strivens M.A., Kioschis P., Dangel A., Cunningham D., Straw R., Weston P., Hunter C., Gilbert M., Fernando S., Goodall K., Kerry G., Greystrong J.S., Clark D., Goerdes M., Blechschmidt K., Rump A., Hinzmann B., Mundy C.R., Miller W., Poustka A., Herman G.E., Rhodes M., Denny P., Rosenthal A., Brown S.D.M.; "Comparative genome sequence analysis of the Bpa/Str region in mouse and man.";
  Q9S181
                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Minimum DB Maximum DB

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Q9vzx5 drosophila
Q9vzx5 drosophila
Q9vzx5 human cycom
Q9y1q1 mus musculu
Q9hks5 thermoplasm
Q9ph51 xylella fas
Q9j511 fowlpox vir

Q9uj28 homo sapien

Ognpa7 homo sapien
Ogy4j5 homo sapien
Ogy4j5 homo sapien
Ogwz92 thermotoga
Ogsyz8 arabidopsis
Ogszx1 rattus norv
Ognwy1 homo sapien
Oz3284 caenorhabdi
O35737 mus musculu
p70333 mus musculu
p70333 mus musculu

Q9np96 homo sapien 052770 pseudomonas Q91291 streptomyce 034558 bacillus su 064101 bacteriopha

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PUTATIVE MEMBRANE PROTEIN.
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Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida
Bacteria; Firmicutes; Actinobacteria;
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Bentley S.D.,
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                              "A set of ordered cosmids and a detailed genetic and the 8 mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL109972; CAB53266.1; -.
                                                                                                                                           SEQUENCE
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PRELIMINALL,
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PROBABLY POSITIONED IN OPERON WITH DOWNSTREAM ORF5.
Bacillus subtilis.
Plasmid pTA1060.
Plasmid pTA1060.
Plasmid pTA1060.
Plasmid pTA1060.
Pacillus Sibrilius PClostridium group;
                                                                                                                                                                                                                                                                                                          O65815 PRELIMINARY; PRT; 520 AA.
O65815; O65814;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 16, Last sequence update)
O1-AAR-2001 (TrEMBLrel. 16, Last annotation update)
CYTOCHROME P450 81B1 (EC 1.14.13.53) (ISOFLAVONE 2'
CYP81B1 OR CYP81B1C OR CYP81B1S.
Helianthus tuberosus (Jerusalem artichoke).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta
         Meijer W.J., Venema G., Bron S.;
"Characterization of single strand origins of
"Lasmids from Bacillus subtilis.";
Nucleic Acids Res. 23:612-619(1995).
EMBL; U32380; AAC44422:1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1423;
                                                                                                                                                                    MEDLINE=98184826; PubMed=9516419; Cabello-Hurtado F., Batard Y., Sawerck-Reichhart D.;
                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-CV. BLANC C
                                                                                                                                                                                                                                                                                   Magnoliophyta; eudicotyle
euasterids II; Asterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95206941; PubMed=7899081; Meijer W.J., Venema G., Bron S.;
                                                                                                                                                      "Cloning, expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 LEIGHMYVL 156
AMINOPURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                   idiplantae; Embryophyta; Tracheophyta; Spe
eudicotyledons; core eudicots; Asteridae;
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66.7%;
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P450 th
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Pred.
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                                                                                                                                                        functional
                                                                                                                                          nctional characterization of catalyzes in-chain hydroxylation
                                                                                                                                                                                                                                                                                        Asteroideae;
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47;
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                                                                               ISOFLAVONES, DAIDZEIN AN
DNES, 2'-HYDROXYDAIDZEIN,
                                                                                                                                                                                     Durst F.,
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09VVF8;
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01-MAY-2000
01-MAY-2000
01-MAR-2001
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                                                                                                                                                                                                                                                                                              Plasmid pXO2.

Plasmid pXO2.

Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.

BCBI_TaxID=1392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTIMICROBIAL COMPOUNDS OF LEGUMES.

-i- ALTERNATIVE PRODUCTS: TWO FORMS; CYP81B1L (SHOWN HERE) AND CYP81B1S; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AJ000478; CAA04117.1; -.
EMBL; AJ000477; CAA04116.1; -.
                                                                                                                                                                                                                  Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF188935; AAF13647.1; -. InterPro; IPR001119; -.
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Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCH
                                                                                                                                                                                                                                                Kumano S., Manter D., Mar
Brown A.E., Jackson P.J.;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Okinaka R.T., Cloud K.,
                                                                                                                                                                                                                                                                                                                                      Bacillus anthracis.
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                               09VVF8
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InterPro;
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0395; SLH; 3.
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O (TrEMBLrel.
1 (TrEMBLrel.
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(TrEMBLrel.
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                              PRELIMINARY;
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58914 MW;
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85.7%;
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66.78;
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16,
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MISSING (IN CYPB1B1S).

MISSING (IN CAA04116).

Y -> S (IN CAA04116).

Y -> Q (IN CAA04116).

P -> Q (IN CAA04116).
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Last sequence update)
Last annotation update)
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                                                                                                                   Score 35; DB
Pred. No. 85;
3; Mismatches
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 sequence update)
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                              1310
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85;
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RA Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RS sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RS sutcon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkva D., Botchan M.R., Bouck J., Brokstein P., Brottier R.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis K.C., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,
RA Burtis K.C., Botchan M.R., Bouck J., Brokstein P., Brottier S.M.,
RA Durbin K.D., Dup L.E., Downes M., Duyan-Rocha S., Dukov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Harris N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Harris N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kechum K.A.,
RA Harris N., Moyan K., Nusson K., Nusskern D.R., Petcleb J.M.,
RA Harris N., Kalush F., Karpen G.H., Ke Z., Morris J., Moshrefi A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
01-NOV-1996 (TrembLrel. 01, Created)
01-NOV-1996 (TrembLrel. 01, Last sequence update)
01-MAR-2001 (TrembLrel. 16, Last annotation update)
MAU GENE CLUSTER, METHYLAMINE DEHYDROGENASE LARGE AND SMALL SUBUNITS,
AND AMICYANIN, (MAUFBEDACJGLMN) GENES, COMPLETE CDS (FRAGMENT).
                                                                                                                                                                           Q49122
Q49122;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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85.7%;
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Pred. No. 2.2e+02;
1; Mismatches (
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006769;
01-JUL-1997 (TrembLrel. 04, C:
01-JUL-1997 (TrembLrel. 04, L:
01-JUN-2000 (TrembLrel. 14, L:
HYPOTHETICAL 69.5 KDA PROTEIN
RV0669C OR MTI376.05.
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Q1-MAR-2001 (TIEMBLI
Q1-MAR-2001 (TIEMBLI
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3-ISOPROPYLMALTATE I
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NCBI_TaxID=408;
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Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Wathwlobacterium group; Methylobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Buchnera).";
J. Bacteriol. 183:0-0(2001).
EMBL; AF197453; AAG31393.1;
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"Vertical Transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-UCAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9;
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                                                                                                                                                                                                                                                                                                                             Similarity 75.06; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 AA;
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
MALTATE DEHYDROGENASE.
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                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
    KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                    40446 MW;
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                                             Last sequence up
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Rature 393:537-544(1998).
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Best Local S
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-i- SIMILARITY: TO SEF
-i- SIMILARITY: TO CHY
EMBL; AC004960; AAC716
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NCBI_TaxID=1773;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                 PF00024;
PF00051;
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6; Conservative
                             ; IPRO00001; -.; IPRO00327; -.; IPRO01324; -.; IPR001314; -.; IPR001314; -.
00024; PAN; 1.
000251; kringle; 4
00089; trypsin; 1
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       CHYMOTRYPSIN
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SERINE PROTEASES, TRYPSIN FAMILY.
CHYMOTRYPSIN SERINE PROTEASE FAMILY
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Pred. No. 1
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1.6e+02;
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PRODOSDM; PD000583; -; 1.
PROSITE; PS00021; KRINGLE_1; U
PROSITE; PS50070; KRINGLE_2; 4
SMART; SM00020; Tryp_SPc; 1.
SMART; SM00020; Tryp_SPc; 1.
Hydrolase; Serine protease.
SEQUENCE 723 AA; 82602 MW;
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082607;
01-NOV-1998 (TrEMBLrel. 0
01-NOV-1998 (TrEMBLrel. 0
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T2L5.9 PROTEIN.
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Geisel C., Smith A., Le T.;
"The sequence of A. thaliana T2L5.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress). 
Eukaryota; Viridiplantae; Embryophyta; Trachec 
Magnoliophyta; eudicotyledons; core eudicots; 
Brassicales; Brassicaceae; Arabidopsis.
  Q9SIM3
                                                                                                                                                                                                                                                                                                                PRINTS; PR00939; C2HCZNFINGER. SMART; SM00343; ZnF_C2HC; 1. Zinc-finger.
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Pfam; PF00098; zf-CCHC; 1.
Pfam; PF00665; rve; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (OCT-1998) to the -/- SIMILARITY: BELONGS TO EMBL; AF096371; AAC62795.1; InterPro; IPR001584; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston
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                                                                                                                                                2 RIGHLYIL 9
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998) to
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55.6%;
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the EMBL/GenBank/DDBJ databases
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Pred. No.
2; Mismatc
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Pred.
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  PRT;
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No.
  1461 AA
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1.9e+02;
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J.3e+02;
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RESULT
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X MEDLINE-Z0083487; PubMed=10617197;

A Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Pujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

A Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,

A Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

A Adams M.D., Freuss D., Nierman W.C., White O., Eisen J.A.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

X Copenhaver G.P., Fraeser C.M., Venter J.C.;

X Salzberg S.L., Fraeser C.M., Venter J.C.;

X "Sequence and analysis of chromosome II of Arabidopsis thaliana.";

Nature 402:761-768(1999).

C --- SIMILARITY: BELONGS TO ZN-FINGER CCHC TYPE FAMILY.
                                   EXEQUENCE FROM N.A.

(C STRAIN-VC-16 / DSM 4304 / ATCC 49558;

(C STRAIN-VC-16 / DSM 4304 / ATCC 49588;

(C STRAIN
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Best Loc
Matches
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028287;
01-JAN-1998
01-JAN-1998
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O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAR-2000 (TrEMBLrel. 16, Last annotation update)
PUTATIVE RETROELEMENT POL POLYPROTEIN.
AT3620460.
AT3620460:
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicates; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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SEQUENCE 1
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InterPro; IPR001878; -.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=2234;
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SMART; SM00343; ZnF_C2HC; 1.
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1461 AA; 162670 MW;
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(TIEMBLIE1. 05, Last sequence update)
(TIEMBLIE1. 13, Last annotation updat)
ING PROTEIN, PUTATIVE.
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2; Mismatches
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3.9e+02;
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hyperthermophilic, sulphate

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RESULT
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ID 24KO
O9Z6KO
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Search completed: June 20, Job time: 344 sec
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                         Query Match 71.3
Best Local Similarity 50.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE000965; AABB9260.1; -.
TIGR; AF1992; -.
InterPro; IPRO02048; -.
PROSITE; PSO0018; EF_HAND; UNKNOWN_1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 313 AA; 34574 MW; 4FDD50CB55BBA
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF103943; AAC97368.1; -
Signal.
SIGNAL 1 38 POTENTIAL.
CHAIN 39 324 FACTORD C PROCESSIONAL
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Q9Z4K0;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
PACTOR C PROTEIN PRECURSOR.
Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
ACBI_TaxID=1911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-80156796; PubMed-6767606;
Biro S., Bekesi I., Vitalis S., Szabo G.;
"A substance effecting differentiation in Streptomyces griseus. Purification and properties.";
Eur. J. Biochem. 103:359-363(1980).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birko 2., Sumegi A., Szeszak F., Vitalis S., Szabo G., Biro S.; "Cloning and sequencing of the factor C gene from Streptomyces griseus 45H.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-45H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=45H;
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272 IEIGHVYI 279
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39 324 F
324 AA; 34555 MW;
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                                                                                                                                                                                                                                                                                        71.7%;
                            2001, 14:10:22
                                                                                                                                                                                                                                                            Score 33; DB 2; Length 324
Pred. No. 1.3e+02;
4; Mismatches 0; Indels
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FACTOR C PROTEIN.
; E5F57BA09D2B4EDB CRC64;
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                                                                                                                                                                                                                                                                                                                     Length 324;
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                          Score
        A_Geneseq_0401:*

| SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Gapop 10.0 , Gapext 0.5
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46
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Copyright (c) 1993 - 2000 Compugen Ltd.
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  R50283

R99345

Y230062

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R07144
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                   Jerusalem artichok
Amino acid sequenc
Exons XV to XVIII
Hepatocyte growth
Sequence of a pept
Nucleic acid trans
                                                                                                                                                                        MAGE-21 nonapeptid
MAGE-21 nonapeptid
Immunogenic peptid
MAGE-12/HLA-B44 tu
                                                                                                                                                                                                                                                                                                     Description
cytotoxic
RESULTANT RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
histocompatability; human leucocyte antigen; probe; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAGE-21 nonapeptide
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R52947	294	R52945	R52944	294	R52942	R52941	R52940	R42062	R39521	R40863	R40862	R25676	R25160	R21976	R20100	R20005	R15623	4	R12792	R10656	W59923	W76690	R99689	R99688	R82685	R57028	$\sim$	70	$\mathbf{r}$	R25677	R21142	R15624	R14307	
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## ALIGNMENTS

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31-AUG-1992;
26-MAR-1993;
07-JUN-1993;
WPI; 1994-100844/12.
N-PSDB; Q44753.
                                                     Boon-falleur T,
                                                                               (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                               30-AUG-1993;
                                                                                                                                                                                                                    WO9405304-A.
                                                                                                                                                                                                                                              Synthetic.
                                       Van Derbruggen P;
                                                                                                                                                                                           17-MAR-1994.
                                                                                                        92US-0938334.
93US-0037230.
93US-0073103.
                                                                                                                                                               93WO-US08157
                                                     De Plaen E,
                                                     Lurquin C,
                                                      Traversari C;
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RESULT REPUBLICANCE OF THE PROPERTY OF THE PRO
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Matches 7
which bind to a HLA molecule on a cell, and provoke lysis by cytolytic T cells (CTLs) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R99345 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nona:peptide derived from tumour rejection antigen precursor - presented by HLA-Al cancer cells, for use in diagnosis or therapy of esp. melanoma and breast cancer.
                                                                                                                 R99343-R99350 represent MAGE nonapeptides, based on the tumour reject antigen region of the full length MAGE sequences. These peptides wer used to design the nonapeptides of the invention (see R99337-R99342),
                                                                                                                                                                                                                                                                                         New nona:peptide(s) that bind
by specific cytolytic T cells,
tumours and to expand T cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA binding peptide; cell lysis; cytolytic T cell; MAGE family; human; tumour rejection antigen precursor; TRA; MAGE-1; tumour; cancer cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                  Example 4; Fig 4; 41pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LUDW-) LUDWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody;
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| 3 vrighly 9
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ly-His-Leu-Tyr is derived from the tumour rejection antigen
encoded by the MAGE-3 gene and presented by HIA-Al. The
de can be used in a vaccine to treat a cancerous condition
HIA-Al subtype cancerous cells. The nucleic acid encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             melanoma; universal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.6%; Score 38; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n E, Gaugler B,
Van Den Eynde B,
                                                                                                                                                                                                                                                                                                                 to HLA molecule
, for diagnosis
                                                                                                                                                                                                                                                                                            in vitro.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell; vaccine; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 15;
3.2e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lurquin C;
Van Der B
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                                                                                                                                                                                                                                                                                                                       and induce lysis treatment of
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RESULT
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptides can also be used therapeutically, to induce a CTL response to tumours (where the peptides are optionally coupled to tumour specific antibodies), or to induce a response by CTLs that are otherwise inactive. The peptide sequences may also be used to expand specific CTLs in vitro for later return to the patient, such as for treating melanoma. Tumour cells can be identified by using DNA encoding the nonapeptides as probes. Non-human cells transformed with the HLA-Al gene and a DNA sequence encoding one of the peptides, can be used to generate CTLs, or to detect the presence of CTLs in human samples. The non-human transformed cells, when polyttansformed, are universal effector cells, and can be used in vaccines, or for treating melanoma or breast cancer.
          Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 on A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral
                                                                                                                                                                                          Claim
                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                         New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9945954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CT; tumour rejection; viral infection; cance prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                    13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                   13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                      (EPIM-)
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                                                                                                                                                                                                                       immunogenic peptides with HLA binding motif, diagnosis of cancers and viral diseases \, -
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                                                                                                                                                                                                                                                                                                                                      EPIMMUNE
                                                                                                                                                                                          Page 54; 150pp;
                                                                                                                                                                                                                                                                                                       Kubo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide having a human leukocyte antigen binding motif #673.
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100.0%;
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                                                                                                                                                                                                                                                                                                     Celis E,
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3.2e+05;
                                                                                                                                                                                                                                                                                                       Grey
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MH
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                                                                                                                                                                                                                                                                                                       Southwood
                                                                                                                                                                                                                                         in treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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The peptides are therefore useful therapeutically

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Best Local S
Matches 7
      This peptide is a tumour rejection antigen presented by a HLA-B44 molecule and derived from a MACE-12 tumour rejection antigen precursor (TRAP). Claimed tumour rejection antigens (W23038-4) are able to bind to HLA-B44 positive cells, making them useful in identifying cells which present HLA-B44 molecules on their surfaces for use in the diagnosis and therapy of cellular abnormalities. The complex of the tumour rejection antigen and HLA molecule provokes a cytolytic T cell response. The tumour rejection antigens, or complexes of tumour rejection antigens and HLA-B44, can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigens and several from cells which present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                                                       Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAGE-12; tumour rejection antigen precursor; TRAP; HLA-B44; human leukocyte antigen B44; cytotoxic T lymphocyte; cancer melanoma; therapy; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W23043;
                                                                                                                                                                                                             Claim 2; Page 51; 74pp;
                                                                                                                                                                                                                                                                                                                                      Van
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W23043 standard; Peptide; 10 AA
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                                                                                                                                                                                                                                                                                                                                                                                (LUDW-) LUDWIG INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                             20-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAGE-12/HLA-B44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-1998
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tumour rejection antigen/HLA complexes
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                                                                                                                                                                                                                                                                                                                                  Bruggen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour rejection antigen.
                                                                                                                                                                                                                                                                                                                                                   Coulie
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                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                   Herman
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                       human leukocyte antigen B44 positive cells for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T lymphocyte; cancer;
                                                                                                                                                                                                                                                                                                                                                   Luescher
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BB
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on their surface,
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                                     The present sequence represents in-chain hydroxylase CYP81B1 of Jerusalem artichoke. CYP81B1 is a microsomal cytochrome P450 that catalyses the omega-2, omega-3 and omega-4 hydroxylation of capric, lauric and myristic acids. The major metabolite is the comega-3-hydroxylated compound. The invention provides isolated nucleic acids (see x58400-06) encoding plant fatty acid hydroxylases (see v05896-902). Also claimed are host cells, transgenic plants and compositions consisting of the plant fatty acid hydroxylase, a process for isolating additional fatty acid hydroxylase genes from a plant, and a process of altering the fatty acid composition in a plant by expressing the plant fatty acid hydroxylase in a transgenic plant. Manipulating or epoxidating a fatty acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid composition in a plant by expressing the plant fatty acid acid content of plants will modify resistance to drought and cattack by insects and other pests. The transgenic plants may also be used as sources of hydroxylated and epoxidized fatty acids useful in the manufacture of e.g. lubricants, ant-slip agents,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                               Batard Y, Benveni
Helvig C, Le Bouq
Werck-Reichhart D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   In-chain hydroxylase; transgenic plant; lipid; hydroxylation; oliseed; vegetable oll; crop protection; Jerusalem artichoke; CYP81B1; cytochrome P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as non-proliferative cancer cells and non-proliferative transfectants.
Sequence
                              plasticisers, coating
                                                                                                                                                                                                                                                                                                                                   Example
                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding plant fatty acid hydroxylases
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-264030/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CNRS ) CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jerusalem artichoke in-chain hydroxylase CYP81B1.
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                                                                                                                                                                                                                                                                                                                                   Fig 20A-B; 157pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Benveniste
Le Bouquin
 505
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                              agents, detergents and surfactants
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Pinot F, Salaun
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RESULT
R25692
ID %2
XX
                                                                                                       Query Match
Best Local Similarity
""thes 7; Conservations
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                      Y34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see X91990) of Chlamydia pneumoniae. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see Y34584-Y35879) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae nucleotides sequences can also be used as immunogenic compositions.
                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of Chlamydia pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                  Griffais
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y34971;
            N25692 standard; Protein; 189
                                                                                                                                                                                                 especially where the vector directs the expression of a neutralising epitope of {\tt C.} pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-NOV-1998;
21-NOV-1997;
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                                                                                           1 VRIGHLYI 8
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ighlyll 46
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                                                                    vrignlyi 33
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                                                                                                                                                                            621 AA;
                                                                                                                   Conservative
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97FR-0014673.
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85.7%;
                                                                                                                             76.1%;
87.5%;
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                                                                                                                              Score 35; DB Pred. No. 38;
            AA.
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                                                                                                                   Mismatches
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Best Local S
Matches 5
                 Synthetic
                                  Transporter system; nucleic acid delivery; carcinogenesis; cardiovascular disease; in
                                                                                                                Y98485 standard; Protein; 697
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                         See also R25676-92,
                                                                                                                                                                                                                                                                 This sequence is made up of exons XV growth factor
                                                                                                                                                                                                                                                                                            Disclosure; Page 22; 28pp; Japanese
                                                                                                                                                                                                                                                                                                             Recombinant human hepatocyte growth factor and DNA encoding it useful for diagnosis and treatment of hepatic disease and transgenic animal prepn.
                                                                                                                                                                                                                                                                                                                                                WPI; 1992-265591/32.
N-PSDB; Q26727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGF; enhance growth; preparing transgenic animals; hepatic disease;
clinical diagnostic reagent; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exons XV to XVIII of human hepatocyte growth factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JAN-1993
                                                            Hepatocyte growth factor Pep 20 used in nucleic acid transporter system.
                                                                              31-JUL-2000
                                                                                               Y98485;
                                                                                                                                                                                                                                                                                                                                                                                                     19-NOV-1990;
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                                                                                                                                                                                                                                                                                                                                                                          (NAKA/) NAKAMURA T
(TOYM ) TOYOBO KK.
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                                                                                                                                                                            1 VRIGHLYIL 9
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| Lrvahlyim
                                                                                                                                                                                             Similarity
5; Conserv
                                                                                                                                                                                                                                        189 AA;
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132..187
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83..131
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48..82
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1..47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= exon XVIII
                                                                                                                                                                                                                                                          Q26713-27
                                                                                                                                                                                                      73.9%;
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                                                                                                                                                                                            ; Score 34; DB; Pred. No. 17; 3; Mismatches
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                                                                                                                                                                                                      DB 17;
                                    infection.
                                                                                                                                                                                                                                                                             XVIII of
                                          gene therapy;
                                                                                                                                                                                                               13;
                                                                                                                                                                                             1;
                                                                                                                                                                                                               Length 189;
                                                                                                                                                                                                                                                                            human hepatocyte
                                                                                                                                                                                              Indels
                                           cancer;
                                                                                                                                                                                              0;
                                                                                                                                                                                            Gaps
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US6033884-A.

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RESULT
Y59030
ID Y51
XX Y51
XX Y51
XX Y51
XX OY51
XX OY51
XX OY6
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complex, consisting of a binding molecule bonded non-covalently to the nucleic acid, and covalently to a surface ligand, and a lytic agent. The binding molecule is spermine or a spermidine derivative. Nucleotide sequences A3663-A3652 and peptide sequences Y9845-Y98500 are used in the construction of the transporter system of the invention. The transporter system is used in gene therapy, particularly to deliver nucleic acids to hepatocytes, muscle cells or bone forming cells, e.g for treating cardiovascular disease, cancer, and infection. The transporter systems are also used to create transgenic animals (as models for human carcinogenesis or disease or for drug testing). Other uses include transforming cells to produce proteins, or transfecting cells in vitro to study the function of the nucleic acid. The use of a surface ligand allows specific targeting of selected cells and tissues. The lytic agent provides for release of the nucleic acid into the cellular interior, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       System for transporting nucleic acid into cells, useful etherapy and for generating transgenic animals, comprises linked to nucleic acid, surface ligand and lytic agent
                                                                                                                                                                                                                                                                                                Nucleic acid transport system; NTS; cell surface receptor; cytosis; nuclear membrane; lysis moiety; transgenic animal; human disease; nucleic acid delivery; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a transporter system for delivering nucleic acid to a cell. The system comprises a nucleic acid binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-281993/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of a peptide ligand Pep20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endosomes, without requiring endosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 23A; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-MAR-2000
      14-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y59030 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                598 lrvahlyim 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VRIGHLYIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 55. 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sparrow J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0855389
93WO-US02725
      9308-0167641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cristiano RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  core 34; DB red. No. 70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or lysosomal degradation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WOO SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith LC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g. in g
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ding agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Query Match
Best Local Similarity
"~+~hes 5; Conserv
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B45838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid transport system (NTS) for Cd delivering nucleic acid into a cell. The NTS contains but is not limited Ct to 5 components: (a) the nucleic acid or a macromolecule to be delivered; (C) a molety that recognizes and binds to a cell surface receptor or Cd antigen or is capable of entering a cell through cytosis; (c) a nucleic acid or macromolecular molecule binding molety; (d) a molety that is CC capable of moving or initiating movement through a nuclear membrane; and/ CC or (e) a lysis molety that tenables the transport of the entire complex CC from the cell surface directly into the cytoplasm of the cell. The NTS CC delivers nucleic acid into the cellular interior as well as the nucleus CC of specific cells. The NTS can be used to treat disorders by targeting CC specific nucleic acid accordingly. The NTS can also be used to create transgenic animals for assessing human disease, such as cancer, in an allows the role of various nucleic acids to be studied by targeting specific expression into specifically targeted tissue culture cells. The CC systs agent within the NTS avoids the problem of endosomal/lysosomal
            14-DEC-1993;
20-MAR-1992;
19-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-MAR-1992;
19-MAR-1993;
14-DEC-1993;
                                                                                                                                        US6150168-A
                                                                                                                                                                                                   Nucleic acid delivery; nucleic acid transporter system; hormone; enzyme; growth factor; clotting factor; apolipoprotein; receptor; drug; oncogene; tumor antigen; tumor suppressor; viral antigen; parasitic antigen; bacterial antigen.
                                                                                                                                                                                                                                                                                                                                                 B45838;
                                                                                                                                                                                                                                                                                                                                                                              B45838 standard; Protein; 697 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 23A; 107pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid transport system, useful for creating transgenic animals for assessing human disease such as cancer in an animal model -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-038262/03
                                                                          05-JUN-1995;
                                                                                                         21-NOV-2000.
                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                 21-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|: ||||:
598 lrvahlyim 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VRIGHLYIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLC,
                                                                                                                                                                                                                                                                                  acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                 transporter system peptide ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-0855389.
93WO-US02725.
93US-0167641.
             93US-0167641.
92US-0855389.
93WO-US02725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                            9508-0460971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gottchalk S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core 34; DB ced. No. 70; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sparrow J,
                                                                                                                                                                                                                                                                                  SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 11
R07144
ID R07144
XX R07144
AC R07144
XX TCF II
XX TCF II
XX HOMO S
YOU WOODLO
PD 20-SEP
XX WOODLO
PD 16-JAN
PR 16-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel system (I) for delivering a nucleic acid CC to a cell, comprising a binding complex comprising a ligand binding CC molecule noncovalently bound to a nucleic acid and covalently linked to a CC surface ligand, and a second binding complex comprising a second binding CC molecule noncovalently bound to a nucleic acid and covalently linked to a nuclear ligand. The complexes are simultaneously bound to the nucleic CC acid. The nucleic acid transporter system can also be used in a method CC for the in vivo targeting of the insertion of DNA into a cell. It can CC also be used in processes for producing transformed cell lines. The CC system can be used to deliver a variety or proteins and polypeptides, CC such as hormones, growth factors, enzymes, clotting factors, and polypeptides, viral antigens, parasitic antigens, and bacterial antigens. The transporter system uses lysis agents to overcome the problems of CC endosomal/lysosomal degradation seen with prior art systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid transporter system for delivering nucleic acid into a cell, useful for delivering proteins and polypeptides to cells, including growth factors, enzymes, hormones, and tumor suppressors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                         P-PSDB; R07144.
                                                                                                Higashio K; Mistuda S;
                                                                                                                                                                                             16-JAN-1990;
03-OCT-1989;
                                                                                                                                                                                                                                                                    03-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                               WO9010651-A
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCF II; glycoprotein; fibroblasts; anticancer agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R07144;
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                                                  WPI; 1990-304990/40
                                                                                                                                             (SNOW)
                                                                                                                                                                                                                                                                                                                  20-SEP-1990
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| lrvahlyim 606
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                                                                                                                                                SNOW
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5; Conserv
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                                                                                                                                                BRAND MILK PRODUCTS
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                                                                                                                                                                                             90JP-0006692.
                                                                                                                                                                                                                                                                    90WO-J000314
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 1...29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor II.
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                                                                                                Shima N; Itagaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cristiano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB Pred. No. 70; 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                Nagao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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R14307
ID R14307
     Дb
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Best Local
  New plasminogen-like growth factor protein - having mitogenic activity on melanocytes, epithelial cells
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The sequence was deduced from the cDNA obtd. from a clone isolated from a cDNA library prepd. from RNA extd. from fibroblast INR-90 cells (ATCC CCL-186). The N-terminal of the alpha chain is unclear. The sequence shows homology to hHGF except between AAS 162 and 166 of this sequence which is absent from the TCF-II sequence. The DNA can be used to produce the TCF II by recombinant DNA technology. TCF II is an anticancer agent and induces differentiation of leukaemia cells, enhances cell-mediated immunity, and accelerates the proliferation of human blood vessel endothelial cells and hepatic parenchymal cells.
WPI; 1991-317957/43.
N-PSDB; Q14182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human glycoprotein having antitumour activity - for inducing differentiation of leukaemia cells and enhancing cell mediated
                                                                                                                                                                                                                                                                                                         Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasminogen-like growth factor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-1992
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                                                                                (USSH ) NAT INST OF HEALTH.
                                                                                                                  14-SEP-1990;
                                                                                                                                               14-SEP-1990;
                                                                                                                                                                                17-SEP-1991.
                                                                                                                                                                                                                US7582063-A
                                                                                                                                                                                                                                                             Active-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitogenic activity; PLGF
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624 lrvahlyim 632
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/note= "mature peptide"
489..490
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Best Local
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The sequence was deduced from a portion of HLC3, one of two clones, (for HLC2 see R15623) isolated from a cDNA library prepd. from mRNA extracted from human leukocytes. HLC2 has almost the same sequence as HLC3 except for five residues (162-166) in HLC2 which do not appear in HLC3. HLC3 shows similar characteristics to the human liver-derived HGF identified in Nature, 342, 440, 1989, but differs at 14 positions in the amino acid sequence. The DNA sequence can be expressed and the resulting protein, recombinant HGF, used in hepatocyte research, esp. into the mechanism of hepatoma, and to prepare anti-HGF antibodies
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                                                                                                                                                                                                                                                                                                                                                 Recombinant human leukocyte-derived hepatocyte growth factor with DNA encoding it, recombinant expression vectors and transformant cells expressing it.
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DB; Q15177.
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5; Conser
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Sakaguchi M,
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Asami
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Pred. No.
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ced. No. 73;
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Tsuda E;
                                                                                                        A human foetal lung fibroblast library was screened with a synthetic probe coding for the N-terminal sequence of TCF-II. A cDNA clone was isolated and sequenced. The coding sequence can be incorporated into a plasmid and transformed into a microorganism for production of TCF-II. The protein itself can be used as a liver cell growth factor or a tumour cell killing factor. See also Q21067-9.
                                                                                                                                                                                                                                                                                                                                                                                                            Key
Region
                                                                                                                                                                             Claim 6; Fig 1; 47pp; Japanese
                                                                                                                                                                                               Prodn. of liver cell growth factor TCF-II - by culture transformant contg. cDNA for TCF-II and deriving from | foetal lung fibroblast cells
                                                                                                                                                                                                                                       WPI; 1992-056868/07
N-PSDB; Q21066.
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490..505
/note= "Beta-chain
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                                                73.98;
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                                                                                                                                                                                                                                                                                                                                                                                                     "Beta-chain N-terminal sequence"
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                                      Score 34; DB Pred. No. 73; 3; Mismatches
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Pred. No.
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Search completed: June 20, 2001, 14:04:01 Job time: 48 sec
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                                                                                                          Query Match 73.9%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                            This sequence represents a recombinant human hepatocyte growth factor. It has physiological activity, and using it enhanced growth of hepatocytes is possible. It is useful as a clinical diagnostic reagent, or a drug for treating hepatic disease.

See also R25676-92, Q26713-27.
                                                                                                                                                                                                                                                                                           Recombinant human hepatocyte growth factor and DNA encoding it useful for diagnosis and treatment of hepatic disease and transgenic animal prepn.
                                                                                                                                                                                                                                                                                                                                                                                                        19-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \ensuremath{\mathsf{HGF}}; enhance growth; preparing transgenic animals; hepatic disease; clinical diagnostic reagent; drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R25677;
                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                     Disclosure; Page 13; 28pp; Japanese.
                                                                                                                                                                                                                                                                                                                                             WPI; 1992-265591/32.
                                                                                                                                                                                                                                                                                                                                                                    (NAKA/) NAKAMURA T. (TOYM ) TOYOBO KK.
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624 lrvahlyim 632
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB seq length: 0
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(MAGE12F).  ldae; Homo.  Plaen E., Brasseur F.,  AGE2 gene.";  OR SEVERAL TYPES,  L CARCINOMA, LUNG  NORMAL TISSUES EXCEPT		Q02335 caenorhabdi P52825 mus musculu P18886 rattus norv Q55934 streptococc P47276 mycoplasma P75081 mycoplasma P75081 mycoplasma P15621 bos taurus P48047 homo sapien Q06647 rattus norv P08368 escherichia P44417 haemophilus P43935 haemophilus

Pfam; PF01454; MAGE; Antigen; Multigene f DOMAIN 40 CONFLICT 10 CONFLICT 187 CONFLICT 300 SEQUENCE 314 AA; This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). EMBL; L18877; AAA19023.1; MIM; 300177; -. InterPro; IPR002190; -. Pfam; PF01454; MAGE; 1. family; 43 10 187 300 34802 Ž. Tumor antigen. POLY-SER.

C -> S (IN REF. 2).

A -> D (IN REF. 2).

P -> S (IN REF. 2).

SW; 3F0787CECD8816A5 CRC64;

FOR TESTES.
SIMILARITY: BELONGS TO THE MAGE FAMILY. STRONG SIMILARITY (90%)

WITH MAGE-2.

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SEQUENCE
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J. EXP. Med. 179;921-930(1994).

-i- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
-i- FUNCTION: NOT KNOWN, THOUGH MAY PLAY A ROLE IN EMBRYONAL
-i- PROGRESSION. ANTIGEN RECOGNIZED ON A MELANOMA BY AUTOLOGOUS
-i- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
-i- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES.
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Gaforio J.J., de
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
MELANOMA-ASSOCIATED ANTIGEN 2 (MAGE-2 ANTIGEN).
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Gaforio J.J., de Plaen E., Lethe B., Brasseur F., I
"Human gene MAGE-3 codes for an antigen recognized
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lia; Eutheria; Primates;
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Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam
Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.
Thaveri A., Ecker J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: MAX BE INVOLVED IN THE SYMTHESIS OF MINOR PHOSPHOLIPI
AND IN MODULATION OF LP3-MEDIATED SIGNAL TRANSDUCTION.
-I-CAPALYTIC ACTIVITY: CTP + PHOSPHATIDATE - PYROPHOSPHATE +
                                                                                                                                    TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIA SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIA SYNTHASE) (CDS) (CTP-PHOSPHATIDATE CYTIDYLYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Cheuk R., Shinn P.
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STRAIN=CV. CC2; TISSUE=Plower, and SiliqueDLINE=97239925; PubMed=9085581;
KOPka J., Ludewig M., Mueller-Roeber B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Embryophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; co
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01315; CDS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X94306; CAA63969.1; -
EMBL; AC003113; AAF70845.1;
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Eukaryota: Viridiplantae: Embryophyta:
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Plant Physiol. 113:997-1002(1997).
                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000374
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mendel; 27238; Arath; 2834; 27238
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SUBCELLULAR LOCATION: INTEGRAL MEMBRAN
SIMILARITY: BELONGS TO THE CDS FAMILY.
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Similarity 7; Conserv
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149
206
246
321
421
  Conservative
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226
266
341
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                          72.0%;
77.8%;
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  POTENTIAL.
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POTENTIAL.
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Pred. No. 8.
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  Mismatches
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dicots; Rosidae; eurosids II;
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Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishi K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138
"Compapan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
"In SIMILARITY: HELONGS TO THE GCPE FAMILY."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlapneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99206606; PubMed=10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCPE_CHLN STANDARD; PRT; 613 AA.

G278B10; Q37Q95;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                             EMBL; AE001621; AAD18517.1; -. EMBL; AE002200; AAF38230.1; -. EMBL; AE002246; BAA98581.1; -- TIGR; CP0383; -.
                                                                                                                                                                                                                    modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae (Chlamydophila pn
Bacteria; Chlamydiales; Chlamydiaceae;
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6 VVYMGHLYI 74
VRIGNLYI
                           VRIGHLYI 9
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                                                                                                                                68308
                                                                     70.0%;
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                                                      Score 35; DB Pred. No. 20; 1; Mismatches
                                                                                                                                40B1F831E02DC6D4 CRC64;
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ae; Chlamydophila
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20;
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y K., Bass S.,
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RY "Mutations in Bartonella bacilliformis gyrB confer resistance to recommermycin Al.";

RT coummermycin Al.";

RT Antimicrob. Agents Chemother. 42:2906-2913(1998).

RL Antimicrob. Agents Chemother. 42:2906-2913(1998).

C. :FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-CONTROL OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.

C. -- CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAGE AND REJOINING OF DOUBLE-STRANDED DNA.

C. -- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE ENGRME FORMS AN AZBZ TETRAMER.

C. -- SIMILABITY: BELONGS TO TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
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Pfam; PF00204; DNA_topoisoII; 1.

Pfam; PF00204; DNA_topoisoII; 1.

PRINTS; PRO0418; TPI2FAMILY.

PROSITE; PS00177; TOPOISOMERASE_II; 1.

PROSITE; PS00177; TOPOISOMERASE_II; 1.

TOPOISOMERASE; ISOMERASE, ATP-binding; Ar

VARIANT 124 124 G -> S (IN C
VARIANT 184 184 R -> Q (IN C
VARIANT 214 214 T -> A (IN C
VARIANT 214 214 T -> A (IN C
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VARIANT 214 214 T -> I (IN C
VARIANT 214 214 T -> I (IN C
                  _HIMAN STANDARD; PRT; 728 AA P14210; O1-JAN-1990 (Rel. 13, Created) O1-AUG-1991 (Rel. 19, Last sequence update) O1-OCT-2000 (Rel. 40, Last annotation update) HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Proteobacteria; alpha
Bartonellaceae; Bartonella.
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Battisti T M
   (HEPATOPOEITIN A)
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T -> A (IN COUMERMYCIN AI MUTANT).
T -> A (IN COUMERMYCIN AI MUTANT).
T -> I (IN COUMERMYCIN AI MUTANT).
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                            ion update)
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HGF OR HPTA.
HOMO Sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria; P
NCBI_TaxID=9606;
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TISSUE-Embryonic fibroblast;

MEDLINE-91334393; PubMed-1831266;

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Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa Asami O., Hagiya M., Nakamura T., Shimizu S.;
"Isolation and expression of CDNA for different forms of growth factor from human leukocyte.";
Biochem. Biophys. Res. Commun. 172:321-327(1990).
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Yoshiyama Y., Arakakai
Nakayama H., Gohda E.,
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Sugimura A., Tashiro K., Shimizu S.;
"Molecular cloning and expression of h
Nature 342:440-443(1989).
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MEDLINE-91340155; PubMed=1831432;
MEDLINE-91340155; PubMed=1831432;
Seki T., Haglya M., Shimonishi M., Nakamura T., Shimizu S.;
"Organization of the human hepatocyte growth factor-encoding gene.";
Gene 102:213-219(1991).
                            Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins in Baker J.B., Godowski P.J.; Godowski 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYDRATE-LINKAGE SITE 476.
MEDLINE=93129192; PubMed=1482348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL SEQUENCE CLEAVAGE SITE.
MEDLINE=91207365; PubMed=1826837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weidner K.M., Arakaki N., Hartmann G.
Rieder H., Fonatsch C., Tsubouchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shimizu N., Hara H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "identification of the N-terminal residue of the heavy chain native and recombinant human hepatocyte growth factor."; Biochem. Biophys. Res. Commun. 175:660-667(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hepatocyte growth
Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Evidence for the identity
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"Molecular cloning and s
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                                                                                                                                                                                                         MEDLINE=92331602;
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affinity
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Gohda E., Kitamura N.,
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M.R., Luis E.A.,
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Hishida T., Daikuhara Y.,
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Ishii T.,
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Pfam; PF00024; PAN; 1.
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Pfam; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS00072; KRINGLE.1; 4.
PROSITE; PS00070; KRINGLE.1; 4.
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor at 2.0-A resolution.", Structure 6:1383-1393(1998).
                                                                                                              GlycoSuiteDB;
MIM; 142409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99036858; PubMed=9817840; Ultsch M., Lokker N.A., Godowski P.J., "Crystal structure of the NEI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor reveals a potential heparin-binding Structure 6:109-116(1998).
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Zhou H., Mazzulla M.J., Kaufman J.D., Stahl S.J., Wi
Rubin J.S., Bottaro D.P., Byrd R.A.;
"The solution structure of the N-terminal domain of
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                                                                                                                                   MEROPS; S01.976
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SIMILARITY: CONTAINS 4 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
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SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED EDICTIVITY.
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CHAIN CHAIN Growth : Signal; SIGNAL

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SEQUENCE FROM N.A., AND C.
C. TISSUE-Mammary fibroblast;
AX MEDILINE-94183257; PubMed-8135822;
AX Sasaki M., Nishio M., Sasaki T., Enami J.;
RA Sasaki M., Mishio M., Sasaki T., Enami J.;
Tidentification of mouse mammary fibroblast-derived mam
"Identification of mouse mammary fibroblast-derived mam
"Thomas hepatocyte growth factor.";
"Thomas hepatocyte growth factor.";
"Thomas hepatocyte growth factor.";
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C08048; 064007; Q61662;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
HEPATOCYTE GROWTH FACTOR PRECURSOR (SC
                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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5; Conserv
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Rodentia;
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PAP.

KRINGLE 1.

KRINGLE 3.

KRINGLE 4.

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Pred. No. 24;
4; Mismatches
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N-LINKED (GI
N-LINKED (GI
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                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                             ion update)
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HK (IN REF. 4)
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(IN REF. 4)
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AC. . .) (POTENTIAL).

AC. . .) (POTENTIAL).
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         MGD; MGI:96079. Hgf.
InterPro; IPR000001; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
InterPro; IPR001314; -.
InterPro; IPR001314; -.
Pfam; PF00024; PAN; 1.
Pfam; PF00051; kringle; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00018; KRINGLE.
PRINTS; PR000722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D10212; BAA01064.1; EMBL; D10213; BAA01065.1; -EMBL; S71816; AAB31855.1; -EMBL; X72307; CAA51054.1; AHSSP; P14210; 2HGF. MGD; MGT:96079; Hgf.
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DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iiu Y., Michalopoulos G.K., Zarnegar R.;

"Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth factor ", Biochim. Blophys. Acta 1216:299-303(1993).

-i- FUNCTION: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOTROPHIC FACTOR, AND ACTS AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL TYPES. IT HAS NO DETECTABLE PROTEASE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94363381; PubMed-8081873;
Lee C.C., Kozak C.A., Yamada K.M.
"Structure, genetic mapping, and
factor gene.";
                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                             Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                    PROSITE; PS00021; KRINGLE_1; 4.
PROSITE; PS50070; KRINGLE_2; 4.
Growth factor; Kringle; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LONG FORM.
SIMILARITY: CONTAINS 4 KRINGLE REGIONS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY
TRYPSIN FAMILY. PLASMINGGEN SUBFAMILY.
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ALTERNATIVE PRODUCTS: A SHORT FORM OF I
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SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED BY A
                                                                                                                                                                                                                                                                                                            Alternative
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33
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32
495
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33
         ALT_INIT.
        INTERCHAIN (BY SIMILARITY).

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N-LINKED (GLCNAC. . .) (POTE:
N-LINKED (GLCNAC. . .) (POTE:
N-LINKED (GLCNAC. . . .) (POTE:
MISSING (IN SHORT ISOFORM).
N -> K (IN REF. 2).
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KRINGLE
KRINGLE
                                                                                                            SERINE PROTEASE-LIKE.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                               HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
HEPATOCYTE GROWTH FACTOR BETA CHAIN.
PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                             BY SIMILARITY
                                                                                                                                                          KRINGLE
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HGF\_MOUSE ID \_MOSE AC 00804 AC 00804 AC 00804 DT 01-NC DT 01-NC DT 01-OC DE HEPAI DE (HEPA GN MGF. OC EUKAS OC EUKAS OC EUKAS NCBI RP SEQUI RP TISSI RA SASA) RA SASA)

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THE REPORT OF THE PROPERTY OF 
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P17945;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=WISTAR: TISSUE=Liver:

WEDLINE=91031482; PubMed=2146117;

Okajima A., Miyazawa K., Kitamura N.;

Okajima A., Miyazawa K., Kitamura N.;

Primary structure of rat hepatocyte growth factor and induction in the structure of rat hepatocyte growth factor and induction in the structure of rat hepatocyte growth factor and induction in the structure of rat hepatocyte parenchymal function: HGF IS A POTENT MITOGEN FOR MATURE PARENCHYMAL HEPATOCYTE CELLS, SEEMS TO BE AN HEPATOCYTE FACTOR AN AS GROWTH FACTOR FOR A BROAD SPECTRUM OF TISSUES AND CELL IT HAS NO DETECTABLE PROTEASE ACTIVITY.

-1- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN LINKED
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STRAIN-WISTAR; TISSUE-Liver;
MEDLINE-90222197; PubMed-2139229;
Toshiro K., Hagiya M., Nishizawa ;
Shimizu S., Nakamura T.;
                                                                                                                                           PIR;
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Deduced primary structure of rat hepatocyte growth factor and expression of the mRNA in rat tissues."; Proc. Natl. Acad. Sci. U.S.A. 87:3200-3204(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEPATOCYTE GROWTH FACTOR PRECURSOR (SCATTER FACTOR) (SF)
                                                  InterPro;
InterPro;
                                                                                                                                                                                           EMBL; D90102; BAA14133.1; EMBL; X54400; CAA38266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-WISTAR; TIS
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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                                                                                        HSSP; P14210; 2HGF.
MEROPS; S01.978; -.
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                           [nterPro;
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SIMILARITY: CONTAINS 4 KRINGLE REGIONS,
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1;
TRYPSIN FAMILY. PLASMINOGEN SUBFAMILY.
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A35644; A35644.
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IPR000001; -. IPR001254; -. IPR001314; -. IPR003014; -.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00024; PAN; 1.
pfam; PF00051; kringle; 4.
pfam; PF00089; trypsin; 1.
pRINTS; PR00118; KRINGLE.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATID_HUMAN STANDARD: PRT; 933 AA. P98198; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Growth
                                                                                             Wiemann S.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + ORTHOPHOSPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00021; KRINGLE_1; 4. PROSITE; PS50070; KRINGLE_2; 4.
                                                                                                                                                                                                                                     "Characterization of cDNA clones selected by the from size-fractionated cDNA libraries from human DNA Res. 6:329-336(1999).
                                                                                                                                                                                                                                                                                                       Ohara O.
                                                                                                                                                                                                                                                                                                                   MEDLINE=20039618; PubMed=10574461;
Hirosawa M., Nagase T., Ishikawa K.-I., Kikuno R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIAA1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                           Ottenwaelder B., Obermaier B., Mewes H.-W.,
                                                                                                                                                                                  rissue=Testis;
                                                                                                                                                                                                     SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VVRIGHLYIL
                           SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY ATPASES). SUBFAMILY IV.
  SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor;
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129
212
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569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        640
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  entry is
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82905
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495
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207
289
384
470
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97
607
295
403
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Primates;
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  copyright.
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY,
HEPATICCYTE GROWTH FACTOR ALPHA CHAIN
HEPATICCYTE GROWTH FACTOR BETA CHAIN
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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  produced
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                                                                                                                                                             Gassenhuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 3.6.1.-) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 728;
                                                                                                                                                                                                                                                              GeneMark analysis brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) (POTENTIAL).
) (POTENTIAL).
) (POTENTIAL).
  through a collaboration
                                                                                                                                                                                                                                                                                                                          Nomura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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Query Match
Best Local Similarity
Tatches 5; Conserv
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                                                                                                                                                                                            004940:
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2000 (Rel. 39, Last annotation update)
10-MAY-2000 (Rel. 39, Last annotation update)
10-MAY-2000 (Rel. 39, Last annotation update)
10-DIGLYCERIDE PHOSPHATIDATE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) (CDP-DG SYNTHETASE).
                                                                                                                                                                                                                                                                                                  _SOLTU
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AL PROSITE;
MEDLINE-97239925; PubMed-9085561;

KEOPKA J., Ludewig M., Mueller-Roeber B.;

"Complementary DNAs encoding eukaryotic-type cytidine-5'-diphosphate-diacylglycerol synthases of two plant species.";

Plant Physiol. 113:997-1002(1997).

-I- FUNCTION: MAY BE INVOLVED IN THE SYNTHESIS OF MINOR PHOSPHOLIPIDS AND IN MODULATION OF IP3-MEDIATED SIGNAL TRANSDUCTION.

-I- CATALYTIC ACTIVITY: CTP + PHOSPHATIDATE = PYROPHOSPHATE +
                                                                                                                                    CDS1.
Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermaרטפיזערער,
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermaרטפיזערער,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
METAL
METAL
SEQUENCE
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                                                                                                                                                                                                                                                                                        CDS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene family.
                                                                                             SEQUENCE FROM N.A. STRAIN=CV. DESIREE;
                                                                                                                           NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                              VIRLGHSYFI 100
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AL137537; CAB70799.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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1 19
0 41
0 41
1 92
1 613
646
646
646
696
718
7755
7755
7755
7751
802
802
8135
135
135
105849
                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                             TISSUE-Leaf
                                                                                                                                                                                                                                                                                                                                                                                                      70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Magnesium; ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW.
                                                                                                                                                                                                                                                                                                                                                                                            ω,
                                                                                                                                                                                                                                                                                                                                                                                                       Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
PHOSPHORYLATION (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
7; CAF60E3574275AC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL. (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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31;
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RESULT
MAG3_HU
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Best Local
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                                                                                                                                                                                                                                                                                                      MAG3_HUMAN
P43357;
01-NOV-1995 (
01-NOV-1995 (
15-JUL-1999 (
Gaugler B., van den Eynde B., van der Bruggen P., Romero P., Gaforio J.J., de Plaen E., Lethe B., Brasseur F., Boon T.; "Human gene MAGE-3 codes for an antigen recognized on a melanoma autologous cytolytic T lymphocytes."; J. Exp. Med. 179:921-930(1994).
                                                                                                                                                                                                                                                                                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-VUL-1999 (Rel. 38, Last annotation update)
MELANOMA-ASSOCIATED ANTIGEN 3 (MAGE-3 ANTIGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM TRANSMEM
                                                                                                                                                                                            MEDLINE=94157413; PubMed=8113684;
                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                  MAGEA3 OR MAGE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                         TISSUE-Blood
                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                    66
                                                                                                                                                                                                                                                                                                                                                                                                               1 VVRIGHLYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDP-DIACYLGLYCEROL.

PATHMAY: PHOSPHOLIFID BIOSYNTHESIS.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: ROOTS AND SINK LEAVES.

SIMILARITY: BELONGS TO THE CDS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                    IIYMGHLYI
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5; Conserv
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206
246
321
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotidyltransferase; Phospholipid biosynthesis;
                                                                                                                                                                                                                                                                       (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                  Chordata;
Primates;
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226
241
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                                                                                                                                                                                                                  MUTAGENESIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB
Pred. No. 22;
3; Mismatches
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POTENTIAL.
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POLY-ARG.
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Catarrhini; Hominidae
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                                 AUTOLOGOUS
  TYPES
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RESULT TRUELES OF THE COLOR OF 
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Best Local S
Matches 6
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P05845;
01-NOV-1988 (Rel. 09
01-JAN-1990 (Rel. 19
01-AUG-1992 (Rel. 2
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                                                                This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               regulatory gene product.";

Nucleic Acids Res. 14:7915-7927(1986).

-!- FUNCTION: TNSABC + TNSD PROMOTE HIGH-FREQUENCY INSERTION OF
INTO A SPECIFIC TARGET SITE KNOWN AS ATT-TN7 WHEREAS TNSABC
PROMOTE LOW-FREQUENCY INSERTION INTO MANY DIFFERENT SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Tn7 transposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-87040763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flores C., Qadri M.I., Lichtenstein C *DNA sequence analysis of five genes; for Tn7 transposition.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-90192166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
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Pfam; PF01454; MAGE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 IGHLYI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transposition: a multigene process.
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       X17693; CAA35687.1;
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el. 23, Last annotation update)
TRANSPOSITION PROTEIN TNSE (PROTEIN
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POLY-SER.
D->A: ABOLISHES HLA-A1 BINDING.
Y->A: ABOLISHES HLA-A1 BINDING
MW; 3F5EB13D1C9946A1 CRC64;
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Pred. No.
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25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification
                                                                                                    http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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Best Local
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P55931;
01-NOV-1997
01-NOV-1997
01-NOV-1997
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence
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PIR; A25543; QCBCD7.
PIR; S12641; S12641.
PIR; S06770; S06770, S06770.
Transposable element; Transposition; DNA recombination; DNA-binding.
DNA_BIND
DNA_BIND
311 330 H-T-H MOTIF (BY SIMILARITY).
SEQUENCE 538 AA; 61211 MW; DE34A3F141A1885B CRC64;
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NON_TER
TRANSIT
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Mammalia; Eutheria;
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                   Local
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                                                                                                                                                                                                                                                                                         Mitochondrion;
 Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S.I., Axtell K.M., Bindoff L.A., Beard S.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Pig).
                                                                                                                                              61
448
551
576
   Conservative
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                                                                                                                                                                                                                                                                                                      Electron
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67590
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468
551
576
579
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607
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85
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75.0%;
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Transit pept
                                                                                          MW.
Pred. No. 50;
1; Mismatches
                                                                                      POTENTIAL.
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
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                                                                                                                                                                                                                  ELECTRON TRANSFER FLAVOPROTEIN-UBIQUINONE OXIDOREDUCTASE.
                                                                                                                                                                                                FAD (ADP PART)
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                                                                                            CRC64;
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(POTENTIAL).
(POTENTIAL).
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e; Transmembrane.
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Sus.
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Best Local Similarity
""" 6; Conservi
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                   SEQUENCE.

SEQUENCE.

TISSUE-pliuitary;

MEDLINE-95354920; Pubmed-7628683;

MEDLINE-95354920; Pubmed-7628683;

NOSO T., Lance V.A., Kawauchi H.;

"Complete amino acid sequence of crocodile growth hormone.";

Gen. Comp. Endocrinol. 98:244-252(1995).

-1- FUNCTION: GROWTH HORMONE PLAYS AN HOPORTANT ROLE IN GROWTH

CONTROL AND INVOLVED IN THE REGULATION OF SEVERAL ANABOLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCKR_XENLA STANDARD; PRT; 619 AA. Q91754; Q1754; Q1754; Q1.NOV-1997 (Rel. 35, Created) Q1.NOV-1997 (Rel. 35, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR). Xenopus laevis (African clawed frog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus laevis (African clawed frog). Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOMA_CRONO STANDARD; PRT; 190 AA P55755; 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation updat SOMATOTROPIN (GROWTH HORMONE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001741; -.
Pfam; PF01380; SIS; 1.
PROSITE; PS01272; GCKR;
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Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen E.;
"Cloning and expression of a Xenopus liver cDNA encoding a fructose-phosphate-insensitive regulatory protein of glucokinase.";
Eur. J. Biochem. 225:43-51(1994).
-I- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE COMPLEX WITH
                                                                                                                                                                                                                                                                                                                          Crocodylus novaeguineae (Crocodile).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archbasauria; Crocodylidae; Crocodylinae; Crocodylus.
NCBI_TaxID-8503;
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   PROCESSES.
SUBCELLULAR LOCATION: SECRETED
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Pfam; PP00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00236; SOMATOTROPIN_2; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
HORMONE; PITULITARY.
DISULFID 163 BY SIMI
DISULFID 180 188
SEQUENCE 190 AA; 22008 MW; 7D8EC
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Q65815 heilanthus
Q9rmz0 bacillus an
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Q9udu6 homo sapien
Q9107 arabidopsis
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01-OCT-2000 (TrEMBLrel. 15, C:
01-OCT-2000 (TrEMBLrel. 15, L:
01-MAR-2001 (TrEMBLrel. 16, L:
MELANOMA ANTIGEN FAMILY A12.
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EMBL; 082671; AAF44789.1; -
InterPro; IPR002190; -
Pfam; PF01454; MAGE; 1.
SEQUENCE 314 AA; 34836 M
    098181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Walker M., Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Knan S., Walker M., Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Knan S., Walker M., Shinn P., Kramenerskaia I., Lenz C., Li J., Liu S., Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;

"Genomic sequence for Arabidopsis thaliana BAC F23N19 from chromosome
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01-MAY-2000
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F23N19.5.
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Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Embryophyta; Trachec

Magnoliophyta; eudicotyledons; core eudicots;

Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudioctyledons; core eudiocts; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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Submitted (MAR-2000) to the EMBL/G
EMBL; AL021/112; CAB16784.1; -.
EMBL; AL161557; CAB79189.1; -.
Mendel; 28363; Arath; 2834; 28363.
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Bevan M., Murphy G.,
Bancroft I., Mewes H.
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                                                                                                            Pfam; PF01148; Cytidylyltrans; PROSITE; PS01315; CDS; 1. SEQUENCE 423 AA; 48247 MW;
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ONTENTAL PROPERTY OF THE STATE 
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Staunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradilip A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradilip A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yelson X.M., Moodaege T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelson S.M., Woodaege T., Worley K.C., Wu D., Smith H.O.,
RA Zheng X.M., Moodaege T., Worley K.C., Wu D., San O., Zheng L.,
RA Yelson S.M., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yelson S.M., Weissenbach J.,
RA Yelson S.M., Wei
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Best Local
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Q9VVF8;
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01-MAY-2000 (TIE
01-MAY-2000 (TIE
CG7692 PROTEIN.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132;
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216
                                                                                   1 VVRIGHLYIL
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                                                                                                                                                                      Score 36; DB Pred. No. 2.2e 2; Mismatches
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2.2e+02
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asley E.M.,
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RESULT Q9S1R5

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Q45454;

Q45454;

Q45454;

TOL-NOV-1996 (TrEMBLrel. 01, Created)

TOL-NOV-1996 (TrEMBLrel. 02, Last sequence update)

TOL-NOV-1998 (TREMBLrel. 08, Last annotation update)

TOL-NOV-1998 (TREMBLREL. 08, Last annotation update)

E PROBABLY POSITIONED IN OPERON WITH DOWNSTREAM ORF5.

Bacillus subtilis.

G Plasmid pTA1060.

C Bacteria; Firmicutes; Bacillus/Clostridium group;

Bacillus/Staphylococcus group; Bacillus.

NC11_TaxID=1423;
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                            MEDLINE=95206941; PubMed=7899081;
Meijer W.J., Venema G., Bron S.;
"Characterization of single strand origins plasmids from Bacillus subtilis.";
Nucleic Acids Res. 23:612-619(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TREMBLIGEL 13, 01-MAY-2000 (TREMBLIGEL 13, 01-MAY-2000 (TREMBLIGEL 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Eichner A., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL, AL109972; CAB53266.1; -.
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-IF03022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bentley S.D., Parkhill Submitted (AUG-1999) to
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                                                                                                                                                                                  EMBL;
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                                                                                                                                                                             ic Acids Res. 23:612:
U32380; AAC44422.1;
                    Similarity 66. 6; Conservative
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e EMBL/GenBank/DDBJ databases.
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                    Score 35; DB Pred. No. 73; 2; Mismatches
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Pred. No. 56;
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                    2;
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                                                                                                                                       DB410B2A7BC51B22
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursler I., Brans A., Braun M., Brignell S.C., Bron S.,
RA Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Browillet S., Enuschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Barrington J., Fabret C., Ferrari E., Foulger D.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Parro V., Pohl T.M., Portetelle D., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
The complete genome sequence of the gram-positive bacterium Bacillus
RT Subtliss ".)
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O1-JAN-1998
O1-JAN-1998
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                                                                                                                                                                                                                                                                          Kunst F., Ogasawara N., Yoshikawa H., Danchin Submitted (NOV-1997) to the EMBL/GenBank/DDBJ EMBL; 299114; CAB13971.1; -. EMBL; 299115; CAB13997.1; -. SEQUENCE 325 AA; 37571 MW; EB73F9970BC5ACC
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Bacteria; Firmicutes; Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98044033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
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256 IVRSGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                             1 VVRIGHLY
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                                                                                                                       6; Conserve
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B (TrEMBLrel. 05,
B (TrEMBLrel. 08,
                                                                                                                       Conservative
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Last sequence update)
Last annotation update)
                                                                                                                   Score 35; DB Pred. No. 79; 1; Mismatches
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                                                                                                                                                                                                                                                                                EB73F9970BC5ACC3 CRC64;
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.D 065815
.D 01-AUG-1998 (TrEMBLrel. 07, Created)
.D 01-AUG-1998 (TrEMBLrel. 16, Last sequence update)
.D 01-AUG-1998 (TrEMBLrel. 16, Last annotation update)
.D 01-AUG-1998 (TrEMBLrel. 16, Last annotation update)
.D 01-AUG-1998 (TrEMBLRel. 16, Last annotation update)
.D 02 CYPOCHROME P450 81B1 (CC 1.14.13.53) (ISOFLAVONE 2'-HYDROXYLASE).
.D 03 CYP81B1 OR CYP81B1S.
.D 04 CYP81B1S.
.D 05 CYP81B1S.
.D 065815
.D 07 CYP81B1S.
.D 07 CYP81B1S.
.D 07 CYP81B1S.
.D 08 CYP81B1S.
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01-AUG-1998
01-AUG-1998
01-AUG-1998
                                                                                                                                                                                          -1- PATHWAY: INVOLVED IN THE BIOSYNTHESIS OF ISOFLAVONOID-E
ANTIMICROBIAL COMPOUNDS OF LEGUMES.
-1- ALTERNATIVE PRODUCTS: TWO FORMS; CYP81BIL (SHOWN HERE)
CYP81BIS; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AJ000478; CAA04417.1; -.
EMBL; AJ000477; CAA04416.1; -.
EMBL; AJ00067; P450; 1.
P2m; PF000185; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage SPBc2.
Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. BLANC COMMUN: TISSUE-TUBER;
MEDLINE-99184826; PubMed-9516419;
Cabello-Hurtado F., Batard Y., Salaun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. seQUENCE 325 AA; 37571 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (AUG-1997) to the EMBL; AF020713; AAC13061.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Karamata D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=66797;
                                                                                                                                                                                                                                                                                                                                                                                                   Werck-Reichhart D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lazarevic V., Duesterhoeft
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(TrEMBLrel.
L 37.6 KDA PR
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Soldo
                                                                                                                                                                                                                                                                                                                                                                                                                     Salaun J.-P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EB73F9970BC5ACC3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
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79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9;
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                                                                                                                                                                 ISOFLAVONOID-DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                     Durst F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                       Pinot F.,
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Brown A.E., Jackson P.J.;
Submitted (NOV-1999) to the EMBL/GenB
EMBL, AF188935, AAF13647.1;
InterPro; IPR007500
Pfam.
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Best Local
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Best Local
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                                                                                                                                                                O06769 PRELIMINARY; PRT; 63:
O06769; O1-JUL-1997 (TIEMBLIEL 04, Created)
O1-JUL-1997 (TIEMBLIEL 04, Last sequence)
O1-JUN-2000 (TIEMBLIEL 14, Last annotated)
HYDOTHETICAL 69.5 KDA PROTEIN.
RV0669C OR MTI376.05.
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobac
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Q9RMZ0;
01-MAY-2000
01-MAY-2000
01-MAR-2001
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VARSPLIC
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SEQUENCE
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SEQUENCE
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Okinaka R.T., Cloud K.,
Kumano S., Manter D., M
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Oxidoreductase;
   SEQUENCE FROM N.A STRAIN=H37RV;
                                                                          Actinomycetales;
NCBI_TaxID=1773;
[1]
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167 VKIGNLYVL
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PF00395; SLH;
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MISSING (IN CAA04116).
Y > S (IN CAA04116).
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Mycobacteriaceae; M
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1.3e+02;
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ACOLe S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
AR Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
AR Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
AD Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
AR Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
ARA Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J.,
ARA Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E.,
ARA Taylor K., Whitchead S., Barrell B G.,
APIOR K., Whitchead S., Whitchead S., Barrell B G.,
APIOR K., Whitchead S., Barrell B G.,
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InterPro; IPRO00027; ...
InterPro; IPRO001254; ...
InterPro; IPRO01254; ...
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InterPro; IPRO00314; ...
Pfam; PF00024; PAN; 1.
Pfam; PF00051; Kringle; 4.
Pfam; PF00089; trypsin; 1.
PFANYS; PR00712; CHYMOTRYPSIN.
PRINTS; PR00018 KRINGLE.
PROSITE; PS00021; KRINGLE_1; UNIPROSITE; PS00020; TYP_SPC; 1.
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SEQUENCE FROM N.A.
COUTTNEY L., Elliot G., Angell S.;
"The sequence of Homo sapiens PAC clone RP5-1098B1.";
"The sequence of Homo sapiens PAC clone RP5-1098B1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9UDU6 PRELIMINARY;
O9UDU6;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Waterston R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (DEC-1999)
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston
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P14210; 1BHT.
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637 AA; 6
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TO SERINE PROTEASES, TRYPSIN FAMILY.
TO CHYMOTRYPSIN SERINE PROTEASE FAMILY (:
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   protease; 82602 |
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Primates;
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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      627B1EF99FAD931B CRC64;
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01-OCT-2000
01-OCT-2000
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Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Conn L., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J Conway A., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C Cheuk R., Shinn P., Brooks S., Buehler E., Chio J., Choi E., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B Lee J., Lenz C., Li J., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO22464; AAR79556.1; SEQUENCE 808 AA; 90243 MW; 6288C800CFIAE04F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ecker
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Best Local Similarity
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Best Local Similarity 50.0%;
Matches 5; Conservative
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Matsushita M.;

Submitted (MAY-1999) to the E
EMBL; AF149013; AAF73131.1; -

InterPro; IPR002111; -

InterPro; IPR002153; -
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Q49122;
Q49122;
Q1-NOV-1996 (TrembLrel. 01, Created)
Q1-NOV-1996 (TrembLrel. 01, Last sequence update)
Q1-MAR-2001 (TrembLrel. 16, Last annotation update)
MAU GENE CLUSTER, METHYLAMINE DEHYDROGENASE LARGE AND SMALL SUBUNITS,
AND AMICYANIN, (MAUFBEDACJGLMN) GENES, COMPLETE CDS (FRAGMENT).
Methylobacterium extorquens.
Bacteria: Protecobacteria; alpha subdivision; Rhizobiaceae group;
Methylobacterium group; Methylobacterium.
                                                                                                                                                                                                                              STRAIN-AM1;

MEDLING-94292425; PubMed-8021187;

Chistoserdov A.Y., Chistoserdova L.V., McIntire W.S., Lidstrom M.E.;

"Genetic organization of the mau gene cluster in Methylobacterium extorquens AM1: complete nucleotide sequence and generation and characteristics of mau mutants.";

J. Bacteriol. 176:4052-4065(1994).

EMBL; L26406; AAB46931.1;

InterPro; IPR0011887;

InterPro; IPR0011887;

Pfam; PF01381; HTH_3; 1.
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SEQUENCE
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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SEQUENCE 1863 AA;
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"ER 139 139
NCE 139 b>...
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Hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Heria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                        Conservative
              June
              20,
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3; Mismatches
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2: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:*

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MAGE-21 nonapeptid
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Immunogenic peptid
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26-MAR-1993;
07-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAGE; nonapeptide; cancer; melanoma; breast cancer; HLA;
histocompatability; human leucocyte antigen; probe; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGE-21 nonapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R50283 standard; Protein; 9 AA.
                                                                                          Van Derbruggen P;
                                                                                                                 Boon-falleur T,
                                                                                                                                                                                                                                                                                                          30-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                       17-MAR-1994.
                                                                                                                                                                                                                                                                                                                                                                                                     WO9405304-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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## ALIGNMENTS

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WPI; 1994-100844/12.
N-PSDB; Q44753.
                                                                                       (LUDW-) LUDWIG INST CANCER RES
                                                                                                                    92US-0938334.
93US-0037230.
93US-0073103.
                                                                                                                                                                                93WO-US08157
                                                          De Plaen E,
                                                          Lurquin C,
                                                          Traversari C;
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RESULT REPUBLIES OF THE RESULT REPUBLIES OF THE RESULT REPUBLIES OF THE RE
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R99343-R99350 represent MAGE nonapeptides, based on the tumour rejection antigen region of the full length MAGE sequences. These peptides were used to design the nonapeptides of the invention. (see R99337-R99342), which bind to a HLA molecule on a cell, and provoke lysis by cytolytic Tells (CTLs) specific for a complex of the HLA molecule and nonapeptide. The nonapeptides can be used diagnostically to identify tumours expressing a particular HLA molecule, or to identify cancer cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nona:peptide derived from tumour rejection antigen precursor - presented by HLA-Al cancer cells, for use in diagnosis or therapy of esp. melanoma and breast cancer.
                                                                                                                                                                                                                                   Example 4; Fig 4; 41pp; English
                                                                                                                                                                                                                                                                                           New nona:peptide(s) that bind to HLA molecule(s) by specific cytolytic T cells, for diagnosis and tumours and to expand T cells in vitro.
                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; melanoma; universal effector cell; vaccine; breast cancer; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGE-21 nonapeptide
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8; Conserv
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)en Eynde B,
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3.2e+05;
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Van Dei
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RESULT
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptides can also be used therapeutically, to induce a CTL response to tumours (where the peptides are optionally coupled to tumour-specific antibodies), or to induce a response by CTLs that are otherwise inactive. The peptide sequences may also be used to expand specific CTLs in vitro for later return to the patient, such as for treating melanoma. Tumour cells can be identified by using DNA encoding the nonapeptides as probes. Non-human cells transformed with the HLA-Al gene and a DNA sequence encoding one of the peptides, can be used to generate CTLs, or to detect the presence of CTLs in human samples. The non-human transformed cells, when polytransformed, are universal effector cells, and can be used in vaccines, or for treating melanoma or breast cancer.
                           Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLs) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and
                                                                                                                                                                                                                                                                         WPI;
are particularly important in tumour rejection and in fighting infections. The peptides are therefore useful therapeutically t
                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09945954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cance prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y46062 standard; Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic
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                                                                                                                                                                                                                         immunogenic peptides with HLA binding modiagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                         1999-551214/46.
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8; Conservative
                                                                                                                                                                                          Page 54; 150pp;
                                                                                                                                                                                                                                                                                                        Kubo RT,
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100.0%;
                                                                                                                                                                                            English.
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Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
This peptide is a tumour rejection antigen presented by a HLA-B44 molecule and derived from a MAGE-12 tumour rejection antigen precursor (TRAP). Claimed tumour rejection antigens (W2308-43) are able to bind to HLA-B44 positive cells, making them useful in identifying cells which present HLA-B44 molecules on their surfaces for use in the diagnosis and therapy of cellular abnormalities. The complex of the tumour rejection antigen and HLA molecule provokes a cytolytic T cell response. The tumour rejection antigens and HLA-B44, can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigens and an antigen and the surface can be used as vaccines to treat disorders characterised by expression of the TRAP molecule such as cancer, especially melanoma. Vaccines can also be prepared from cells which present the tumour rejection antigen/HLA complexes on their surface, such
                                                                                                                                                                                                                                                                                   Tumour rejection antigens presented by molecules - useful to identify HLA-B44 and therapy of cellular abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       melanoma; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGE-12; tumour rejection antigen precursor; TRAP; HLA-B44; human leukocyte antigen B44; cytotoxic T lymphocyte; cancer
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                                                                                                                                                                                                                                                   Claim
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Van Der Bruggen
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                                                                                                                                                                                                                                                 2; Page 51; 74pp;
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Herman
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Pred. No.
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                                                                                                                                                                                                                                                                                                   human leukocyte antigen B44 positive cells for diagnosis
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       CC r45390 to y48214 represent specifically claimed immunogenic peptides CC having a human major histocompatibility complex (MHC) Class I (also CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B-or C) and induce a cytotoxic T cell CC response against the antigen from which the peptide is derived.

CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are CC normally induced by an antigen in the form of a peptide fragment bound CC are particularly important in tumour rejection and in fighting viral CC infections. The peptides are therefore useful therapeutically to treat CC or prevent viral infections and cancers in mammals (especially humans) CC protoxiate cancer, hepatitis B and C. AIDS, and renal carcinoma.

CC They can be administered as vaccines to elicit an immune response in CC individuals susceptible or otherwise at risk of viral infection or CC useful diagnostically, and can be used to induce a cytotoxic T cell CC produce CTLs ex vivo for infusion back into a patient. The peptide e.g. to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as non-proliferative cancer cells and non-proliferative transfectants.
                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                   New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTI; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                        Claim 1; Page 104; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIM-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide having a human leukocyte antigen binding motif #1954.
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3 vvrighly 10
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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Pred. No.
immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                     viral
                                                                                                                                                                                                                                                                                                                                                                                                            Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                       l diseases -
                                                                                                                                                                                                                                                                                                                                                   binding
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                                                                                                                                                                                                                                                                                                                                                                                                            ,MH
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                                                                                                                                                                                                                                                                                                                                                                                                            Southwood
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05-MAR 1999

09-MAR 1999

25-MAR 1999

25-MAR 1999

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26-APR 1999

27-APR 1999

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21-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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8; Conservative
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9908-012548
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9908-0128714
9908-0128045
9908-0130077
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Pred. No. 0.17;
0; Mismatches
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110-JUN-1999
110-JUN-
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9908-0138844
9908-0138452
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06-AUG-1999; 06-AUG-1999; 09-AUG-1999; 09-AUG-1999; 10-AUG-1999;

13-AUG-1999; 16-AUG-1999; 17-AUG-1999;

11-AUG-1999; 12-AUG-1999; 13-AUG-1999;

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Gaps

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Query Match
Best Local Similarity
                                 990S-015066
990S-0151065
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990S-0151066
990S-0151375
990S-0152373
990S-0153758
990S-0154739
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990S-0155569
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990S-0160814
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990S-0161360
990S-0161361
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990S-0147463

990S-0147935

990S-0148171

990S-014831

990S-014834

990S-014866

990S-014966

990S-0149175

990S-0149723

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990S-014973

990S-014993

990S-014993

990S-014993
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77.8%;
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Pred.
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DB
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            Length 363;
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28-SEP-1999
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21-CCT-1999
22-SEP-1999
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24-SEP-1999
25-CCT-1999
26-CCT-1999
27-CCT-1999

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Matches
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VVRIGHLYI 9
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                                           Similarity 66. 6; Conservative
                                                                                    9908-0148565
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                                                      72.0%;
66.7%;
                                          Score 36; DB Pred. No. 15; 2; Mismatches
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                                                               Length 365;
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RESULT
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match
Best Local Similarity 77.8%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVRIGHLYI 9

Qy 1 VVRIGHLYI 9

Db 66 vvymghlyi 74
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Search completed: June 20, 2001, 14:04:02 Job time: 49 sec

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Title:
Perfect score:
Sequence:
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re greater than or equal to the score of the result being printed,
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gcpE protein CP038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
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## ALIGNMENTS

C;Species: Homo\_saplens (man)
C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 18-Feb-2000
C;Accession: T34519; JC2362; PH1295
R;De Smet, C; Lurquin, C; van der Bruggen, P; De Plaen, E; Brasseur, F; Boon, T.
Immunogenetics 39, 121-129, 1994
A;Title: Sequence and expression pattern of the human MAGE2 gene.
A; Reference number: I54519; MOID:94102805
A; Accession: I54519

melanoma antigen MAGE-12 - human N;Alternate names: MAGE 21 protei

protein

£54519

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-314 <DES>
A;Cross-references: GB:L18877: NID:g499345; PIDN:AAA19023.1; PID:g499346
A;Cross-references: GB:L18877: NID:g499345; PIDN:AAA19023.1; PID:g499346
B;Ching, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Blochen. Blophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935
A;Accession: JC2362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>
A;Residues: 1-9,'S',11-186,'D',188-299,'S',301-314 <DIN>
A;Residues: 1-9,'S',11-186,'D',188-299,'B',1902
A;Traversari, C.; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van. P.
J. Exp. Med. 176, 143-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytoly A;Reference number: PH1294; MUID:93018875
A;Accession: PH1294; MUID:93018875
                        RESULT
B96652
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C;Superfamily: tumor associated protein MAGE
F;168-176/Region: HLA-Al binding #status predicted
protein F23N19.5 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: MAGEA12; MAGE12; MAGE-12f
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A; Residues: 168-176 <TRA>
                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                       170 VRIGHLYIL 178
                                                                                                                                                                                          1 VRIGHLYIL
                                                                                                                                                                                                                                             similarity 100.0%;
9; Conservative 0
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                                                                                                                                                                                                                                                   0;
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Pred. No. 0.085;
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                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                   Length 314;
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                                                                                                                                                                                                                                                   0;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: B96652
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, I ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, N.; Li, J., J., Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Mccession: B96652
A;Status: preliminary
A:Malconle two. Nan
hypothetical protein 4.60 - Bacillus subtilis plasmid pTA1060 C; Species: Bacillus subtilis C; Species: Bacillus subtilis C; Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Nov-1999 C; Accession: I40565
R; Meijer, W.J.; Venema, G.; Bron, S.
Nucleic Acids Res. 23, 612-619, 1995
A; Title: Characterization of single strand origins of cryptic rolling-circle plasmids A; Reference number: I40549; MUID:95206941
A; Accession: I40565
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T37141 R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, August 1999
                                                                                                                                                                                                                            RESULT
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A; Accession: T37141
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A:Gene: F23N19.5
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A; Residues: 1-234 <HAR>
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A; Map position: 1
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A; Residues: 1-233 <STO>
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Best Local
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Best Local :
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5; Conser
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85.7%;
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Pred. No. 11;
3; Mismatches
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11;
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                                                          A; DEGLUS. FILE. DNA
A; MOLECULE type: DNA
A; Residues: 1-613 <STO>
A; Cross-references: GB:BA000008; NID:g8978745; PIDN:BAA98581.1; GSPDB:GN00142
A; Cross-references: GB:BA000008; NID:g8978745; PIDN:BAA98581.1; GSPDB:GN00142
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#text\_change 02-Mar-2001

pneumoniae

F.; Ouchi, K.; Shiba,

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A; Molecule type: DNA
A; Residues: 1-305 <RES>
A; Cross-references: EMBL:U32380; NID:g1049123; PIDN:AAC44422.1; PID:g1049128
A:Experimental source: plasmid pTA1060
C; Genetics:
                                                                                                                 A;Description: specifically catalyzes the hydroxylation of medium chain saturated fat C;Superfamily: human cytochrome p450 CYP2D6; cytochrome p450 homology C;Keywords: chromoprotein; fatty acid metabolism; heme; iron; metalloprotein; oxidore F;301-463/bomain: cytochrome p450 homology <P45> F;441/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome P450 (EC 1.14....) 81Blc - Jerusalem artichoke
C;Species: Helianthus tuberosus (Jerusalem artichoke)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Feb-2001
C;Accession: T10896
Query Match
Best Local Similarity
Watches 6; Conserva
                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-505 <CAB>
                                                                                                                                                                                                                                                                                                                                                                                                    J. BJOl. Chem. 273, 7260-7267, 1998
A;TILLe: Cloning, expression in yeast and functional characterization of CYP81B1, a p
A;Reference number: Z17204; MUID:98184826
A;Accession: T10896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Genome: plasmid
C; Superfamily: Bac
                                                                                                                                                                                                                                A; Gene: CYP81B1c
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Cabello-Hurtado, F.; Batard, Y.; Salaun, J.; Durst, F.; Pinot, J. Biol. Chem. 273, 7260-7267, 1998
                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:AJ000477; NID:g3059128; PIDN:CAA04116.1; A;Experimental source: cv. blanc commun
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Best Local Similarity
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66.7%;
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85.7%;
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Pred. No.
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Pred. No.
                       Mismatches
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                                           DB
26;
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                       Indels
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                    0;
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; GentLes, S.; Hamlin, N.; H. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Decliphering the biology of Mycobacterium tuberculosis from the comple A;Reference number: A70500; MUID:98295987
A;Accession: H70535
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001621; GB:AE001363; NID:g4376641; PIDN:AAD18517.1; PID:g437665 A;Experimental source: strain CWL029 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcpE protein CP0383 [imported] - Chlamydophila pneumc C;Specles: Chlamydophila pneumoniae, Chlamydia pneumc C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #t C;Accession: E72087; D81582
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Nature Genet. 21, 385-389, 1999
                                                                                                                                           A;Cross-references: GB:295972; GB:AL123456; NID:g3261790; A;Experimental source: strain H37Rv C;Genetics:
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                                                                                              A; Gene: Rv0669
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein Rv0669c - Mycobacterium tuberculosis (strain H37RV) c;Species: Mycobacterium tuberculosis C;Decies: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: H70535
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A;Residues: 1-613 <REA>
A;Cross-references: GB:AE002200; GB:AE002161; NID:g7189305; PIDN:AAF38230.1;
A;Experimental source: strain AR39, HL cells
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A; Residues: 1-637 <COL>
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A; Residues: 1-613 <ARN>
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;Species: Chlamydophila pneumoniae, Chlamydda pneumoniae
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
;Accession: E72087; D81582
    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 87.17; Conservative
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                                                                                              Mycobacterium tuberculosis hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.1%;
87.5%;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۳.
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Pred. No.
    Score 34;
Pred. No.
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DB
54;
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                           Length
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                                                                                                                                                                                        PIDN:CAB09388.1; PID:g2143290
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A; Accession: JU0333
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                                                                                                                A; Molecule type: mRNA
A; Residues: 1-161,167-728 <RUB>
A; Cross-references: GB: M55379
                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-728 <MIY>
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A; Residues: 1-161,167-728 <SE4>
A; Cross references: EMBL: X16323
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A;Accession: A36677
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A; Residues: 1-728 <SE3>
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A; Residues: 1-728 <SEK>
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A; Accession: JH0579
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                                                                                                                                                                                        A; Accession: A39006
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A; Residues: 1-728 <WEI>
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A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki,
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte
A;Reference number: A33512; MUID:89392017
A;Accession: A33512
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A;Title: Organization of the human hepatocyte growth factor-encoding
A:Reference number: JH0579; MUID:91340155
A;Experimental source: embryonic lung R;Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, Biochem. Biophys. Res. Commun. 175, 660-667, 1991 A;Title: Identification of the N-terminal residue of the heavy A;Reference number: PH0114; MUID:91207365
                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846 R;Rbbin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991 Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991 A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepat A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepat A;Reference number: A39006; MUID:91110540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M73239; NID:g337935; PIDN:AAA64239.1; PID:g337936
R;Seki, T.; Thara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagi
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth
A;Reference number: A36677; MUID:91025062
A;Accession: B36677;
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A; Mesidues: 1-481, 'RT', 484-728 <SE2>
A; Residues: 1-481, 'RT', 484-728 <SE2>
R; Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A; Title: Evidence for the identity of human scatter factor & A; Reference number: A41140; MUID: 91334393
A; Accession: A41140
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A;Note: the authors translated the codon GAA for residue 662 as Gly
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
submitted to JTPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding
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N,Alternate names: hepapoietin A; scatter factor
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;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
;)Accession: JH0579, JU0333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796;
;Seki, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
tene 102, 213-219, 1991
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                                                chain
                                                                                                                            S.; Kondo,
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A; Description: stimulates mitosis of hepatocytes and other cells
A; Note: does not have proteinase activity
C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
F; 13-1/Domain: signal sequence #status predicted <SIG>
F; 32-494/495-728/Product: hepatocyte growth factor #status experimental <MAT>
F; 32-494/Domain: alpha chain #status experimental <ACH>
F; 128-206/Domain: kringle homology <KR2>
F; 11-289/Domain: kringle homology <KR2>
F; 391-489/Domain: kringle homology <KR3>
F; 391-469/Domain: kringle homology <KR4>
F; 395-718/Domain: trypsin homology <KR4>
F; 495-718/Domain: trypsin homology <KR4>
F; 495-718/Domain: trypsin homology <KR4>
F; 32/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F; 32/Modified site: pyrrolidone carboxylic acid (Gln) (covalent) #status predicted
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A;Molecule type: mRNA
A;Residues: 1-288,'ET' <MIY2>
A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
A;Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
A;Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A;Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibra;Reference number: 152253; MUID:g2062058
A;Accession: 152253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNĀ A; Residues: 1-288 / ET / CHAR> A; Residues: 1-288 / ET / CHAR> A; Cross-references: GB:L02931; NID:g184033; PIDN:AAA52649.1; R; Miyazawa / K.; Kitamura / A.; Naka / D.; Kitamura / N. Eur. J. Biochem. 197, 15-22, 1991 a; Title: An alternatively processed mRNA generated from human A; Reference number: S15443; MUID:91200041
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A;Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact A;Reference number: 159214; MUID:93087571
A;Accession: I59214
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'
A;Residues: 86-91;329-344;356-363,'XX',366-370;425-434;442-447,'X',449-450;543-546,'
R;Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; 1
Nature 342, 440-443, 1989
A;Title: Molecular cloning and expression of human hepatocyte growth factor.
A;Reference number: S06794; MUID:90066676
A;Recession: S06794
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A;Title: Scatter factor: molecular characteristics
A;Reference number: A37796; MUID:91035621
A;Accession: A37796
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A;Map position: 7q21.1 rq21.1
A;Introns: 30/1, 85/2; 123/1; 161/2; 209/1; 249/2;
C;Complex: disulfide-bonded heterodimer of chains
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A; Note: the authors translated the codon CAG for residue 727 as Glu
A; Note: part of this sequence, including the amino end of both the a
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A;Residues: 1-31,'HK',34-77,'N',79-292,'V',294-299,'M',301-316,'A',318-335,'K',337-386,
A;Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
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R; Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier,
J. Cell Biol. 11, 2097-2108, 1990
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A; Molecule type:
A; Residues: 32-43
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A; Residues: 161-166 <SHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB:S62561; NID:g237996; PIDN: AAB20169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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derived
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A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Reywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle;
F;1-32/Domain: signal sequence #status predicted <SIG>
F;16-495/Droduct: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: kringle homology <KR4>
F;496-728/Domain: trypsin homology <KR4>
F;393-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte
A; Reference number: S13211; MUID:91031482
A; Accession: S13211
            N;Alternate names: hepapoietin A; scatter factor C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000 C;Date: 03-Mar-1995 #sequence_revision 26-May-1994 #text_change 16-Jun-2000 C;Accession: JC2117; PC2064; A60185; S43416; S45521; S17173; S10966; I48758; R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-728 < TAS>
A; Cross-references: GB:D90102; GB:M32987; NII
A; Cross-references: GB:D90102; GB:M32987; NII
A; Note: the authors translated the codon GAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Tashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Naka
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of
A;Reference number: A35644; MUID:90222197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: hepapoietin A; scatter factor C;Species: Rattus norvegicus (Norway rat) C;Decies: Resep-1900 #seguence_revision 18-Nov-1992 #text_change 21-Jul-2000 C;Accession: A35644; S13211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-728 < OKA>
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A; Accession: A35644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X54400; NID:g56353; PIDN:CAA38266.1; PID:g4539554 C;Complex: disulfide-bonded heterodimer of chains derived from the same pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
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5; Conser
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T.; Enami, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34;
Pred. No.
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62;
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A;Title: Hepatocytes and scatter factor.
A;Reference number: $10966; MUID:90326152
A;Accession: $10966
A;Accession: $20,000
A;Accession: $20,000
A;Accession: $20,000
A;Accession: $148758
A;Accession: $14875
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A; Reference number: $45521
A; Accession: $45521
A; Accession: $45521
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-563,'H',565-728 <LI2>
A; Cross-references: EMBL:X72307
A; Cross-reference in EMBL:X72307
A; Cross-reference in EMBL:X72307
A; Reference number: $17173; MUID:91354223
A; Accession: $17173
A; Accession: $17173
A; Accession: $17173
A; Accession: $17173; MUID:91354223

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A; Description: The sequence of A. thaliana T2L5.
A; Reference number: 214470
A; Accession: T01956
A; Status: translated from GB/EMBL/DDBT
A; Molecula From.
                                                                                                                                                                                                                                                                                                                                  R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                        probable retroelement pol polyprotein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001 C;Accession: E84589
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E84589
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F;496-719/Domain: trypsin homology <TRX>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted F;488-607/Disulfide bonds: #status predicted
                                                                                                       A;Gene: At2g20460
A;Map position: 2
C;Superfamily: re
                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1461 <STO>
A; Cross-references: GB:AE002093; NID:g4586028;
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A; Note: T2L5.9
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A;Residues: 1-1244 <GEI>
A;Cross-references: MMBL:AF096371; NID:g3695386; PID:g3695393
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T01956
R; Geisel, C.; Smith, A.; Le,
submitted to the EMBL Data L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T2L5.9 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999
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                                                                                                                                                                                                                                                                                                A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A; Reference number: A84420; MUID: 20083487
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                                                                                                          retrovirus-related
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                       73.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
75
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Pred. No. 62;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2; Lo
Pred. No. 1.1e+02;
2; Mismatches 0;
                       Score 34;
Pred. No.
                                                                                                          polyprotein
                                         BB
.3e+02;
0;
                                                                                                                                                                                             PIDN: AAD25646.1; GSPDB: GN00139
                                              2:
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                                           Length 1461;
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Similarity 6; Conserv

Mismatches

0;

Gaps

0

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melanoma antigen MAGE-3 - human
N;Alternate names: MAGE 3 protein
C;Species: Romo sapiens (man)
C;Decies: Homo sapiens (man)
C;Decies: Homo sapiens (man)
C;Accession: JC2361; PH1296; I38438
R;Ding, M.; Beck, R.J.; Keller, C.J.; Fenton, R.G.
Biochem. Biophys. Res. Commun. 202, 549-555, 1994
A;Title: Cloning and analysis of MAGE-1-related genes.
A;Reference number: JC2358; MUID:94311935
A;Accession: JC2358; MUID:94311935
A;Accession: JC2358; MUID:94311935
A;Accession: JC2358; MUID:94311935
A;Traversari, C; van der Bruggen, P.; Luescher, I.F.; Lurquin, C.; Chomez, P.; Van Pel,
J. Exp. Med. 176, 1453-1457, 1992
A;Title: A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-Al by cytolytic
A;Reference number: PH1294; MUID:93018875
A;Molecule type: DNA
A;Residues: 168-176 <TRA>
A;Residues: 168-176 <TRA>
A;Residues: 179, 221-930. 1994
J. Exp. Med. 179, 221-930. 1994
J. Exp. Med. 179, 221-930. 1994
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G69498

calcium-binding protein homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C;Accession: 669498

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Gloddek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed

A;Accession: G69498

A;Accession: G69498

A;Accession: G69498

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-313 < KLE>

A;Cross-references: GB:AE000965; GB:AE000782; NID:92689288; PIDN:AAB89260.1; PID:9264854
                                                                                                                                                                                 R;Gaugler, B.; Van den Eynde, B.; van der Bruggen, P.; Romero, P.; Gaforio, J.J.; De Pl J. Exp. Med. 179, 921-930, 1994
A;Title: Human gene MAGE-3 codes for an antigen recognized on a melanoma by autologous A;Reference number: 138438; MUID:94157413
A;Accession: 138438
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-314 <RES>
A:Cross-references: EMBL:U03735; NID:g468825; PIDN:AAA17446.1; PID:g468826
C;Genetics:
A:Gene: MAGE-3
C;Superfamily: tumor associated protein MAGE
F;468-176/Region: HLA-Al binding #status predicted
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 IEIGHVYI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 RIGNLYVL 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VRIGHLYI 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 2; Length 313;
pred. No. 39;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Query Match 71.7%; Score 33; DB 2; Length 314; Best Local Similarity 100.0%; Pred. No. 39; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 3 IGHLYI 8

Db 172 IGHLYI 177
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Search completed: June 20, 2001, 14:04:33 Job time: 80 sec